

US08963288 (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MPern_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Jul 10 12:41:40 1998; MasPar time 53.01 Seconds

Tabular output not generated. 152.949 Million cell updates/sec

Title: >US08963288.SEQ
Description: (1-9) from us08963288.seq
Perfect Score: 9
N.A. Sequence: 1 ttctgagaa 9
Comp: " " aagactcct

Scoring table: TABLE default
Gap 10

Mmatch STD : Dbase 0; Query 0

Searched: 1387090 seqs, 450406388 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-pending
1:P9 2:U6000 3:U6001 4:U6002 5:U6003 6:U6004 7:U6005
8:U6006 9:U6007 10:U6008 11:U7 12:U80 13:U81 14:U82
15:U83 16:U84 17:U84B 18:U85 19:U86 20:U87 21:U88
22:U89 23:U90A 24:U90B 25:U91 26:NEWP 27:NEW06 28:NEW08
29:NEW09

Statistics: Mean 4.896; Variance 1.309; scale 3.740

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB, ID	Description	Pred. No.
c 1	100.0	9	20 14	US-08-227- Sequence 11, Applicant	4.09e+03
c 2	100.0	9	32 1	PCT-US97-2 Sequence 6, Applicant	4.09e+03
c 3	100.0	9	33 23	US-09-024- Sequence 146, Applicant	4.09e+03
c 4	100.0	9	192 22	US-08-997- Sequence 3, Applicant	4.09e+03
c 5	100.0	9	214 17	US-08-451- Sequence 762, Applicant	4.09e+03
c 6	100.0	9	221 14	US-08-221- Sequence 409, Applicant	4.09e+03
c 7	100.0	9	221 27	US-60-090- Sequence 370, Applicant	4.09e+03

c 8	100.0	9	255 10	US-60-089- Sequence 209, Applicant	4.09e+03
c 9	100.0	9	269 20	US-08-757- Sequence 279, Applicant	4.09e+03
c 10	100.0	9	284 10	US-60-089- Sequence 3218, Applicant	4.09e+03
c 11	100.0	9	291 27	US-60-090- Sequence 1196, Applicant	4.09e+03
c 12	100.0	9	293 10	US-60-087- Sequence 139, Applicant	4.09e+03
c 13	100.0	9	305 23	US-09-041- Sequence 1985, Applicant	4.09e+03
c 14	100.0	9	327 17	US-08-451- Sequence 2503, Applicant	4.09e+03
c 15	100.0	9	388 27	US-60-090- Sequence 369, Applicant	4.09e+03
c 16	100.0	9	463 22	US-08-916- Sequence 13, Applicant	4.09e+03
c 17	100.0	9	477 22	US-08-916- Sequence 16, Applicant	4.09e+03
c 18	100.0	9	510 14	US-08-276- Sequence 12341, Applicant	4.09e+03
c 19	100.0	9	621 10	US-60-082- Sequence 4380, Applicant	4.09e+03
c 20	100.0	9	676 10	US-60-082- Sequence 379, Applicant	4.09e+03
c 21	100.0	9	698 23	US-09-040- Sequence 2, Applicant	4.09e+03
c 22	100.0	9	1116 10	US-60-087- Sequence 3, Applicant	4.09e+03
c 23	100.0	9	1133 29	US-09-103- Sequence 5, Applicant	4.09e+03
c 24	100.0	9	1610 29	US-09-103- Sequence 6, Applicant	4.09e+03
c 25	100.0	9	1933 29	US-09-104- Sequence 1, Applicant	4.09e+03
c 26	100.0	9	1933 29	US-09-104- Sequence 1, Applicant	4.09e+03
c 27	100.0	9	2015 27	US-60-090- Sequence 113, Applicant	4.09e+03
c 28	100.0	9	2144 28	US-08-876- Sequence 3, Applicant	4.09e+03
c 29	100.0	9	2144 28	US-08-876- Sequence 1, Applicant	4.09e+03
c 30	100.0	9	2214 23	US-09-004- Sequence 11, Applicant	4.09e+03
c 31	100.0	9	2771 17	US-08-468- Sequence 5, Applicant	4.09e+03
c 32	100.0	9	3182 1	PCT-US94-0 Sequence 12, Applicant	4.09e+03
c 33	100.0	9	4476 21	US-08-801- Sequence 2, Applicant	4.09e+03
c 34	100.0	9	5140 21	US-08-825- Sequence 20, Applicant	4.09e+03
c 35	100.0	9	5163 1	PCT-US97-1 Sequence 1, Applicant	4.09e+03
c 36	100.0	9	5173 21	US-08-801- Sequence 2, Applicant	4.09e+03
c 37	100.0	9	5251 28	US-08-702- Sequence 8, Applicant	4.09e+03
c 38	100.0	9	5538 14	US-08-231- Sequence 55, Applicant	4.09e+03
c 39	100.0	9	6571 28	US-08-702- Sequence 9, Applicant	4.09e+03
c 40	100.0	9	6571 28	US-08-702- Sequence 10, Applicant	4.09e+03
c 41	100.0	9	6826 23	US-09-024- Sequence 8, Applicant	4.09e+03
c 42	100.0	9	6896 19	US-08-627- Sequence 6, Applicant	4.09e+03
c 43	100.0	9	7624 20	US-60-725- Sequence 30, Applicant	4.09e+03
c 44	100.0	9	10093 8	US-60-068- Sequence 313, Applicant	4.09e+03
c 45	100.0	9	21715 15	US-08-308- Sequence 14, Applicant	4.09e+03

ALIGNMENTS

RESULT 1
ID US-08-227-357-11 STANDARD; DNA; UNC; 20 BP.
AC xxxxxx
DE Sequence 11, Application US/08227357
CC GENERAL INFORMATION:
CC APPLICANT: Diasio, Robert B.
CC APPLICANT: Lu, Zhihong
CC APPLICANT: Zhang, Ruiwen
CC APPLICANT: Johnson, Martin
CC APPLICANT: Cheng, Xiang
CC TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USE IN
CC TITLE OF INVENTION: DETECTING DIHYDROPRYIMIDINE DEHYDROGENASE (DPD) AND IN
CC TITLE OF INVENTION: OPTIMIZING 5-FLUOROURACIL TREATMENT
CC NUMBER OF SEQUENCES: 15
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: Arnold, White & Durkee
CC STREET: P. O. Box 4433
CC CITY: Houston
CC STATE: TX
CC COUNTRY: USA

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3

CC ZIP: 71210-4433
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/227,357
CC FILING DATE: 13-APR-1994
CC CLASSIFICATION: 514
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Wilson, Mark B.
CC REGISTRATION NUMBER: 37,259
CC REFERENCE/DOCKET NUMBER: UOAB:016/WTM
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 713-787-1400
CC TELEFAX: 713-789-2679
CC INFORMATION FOR SEQ ID NO: 11:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 20 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
SQ SEQUENCE 20 BP; 7 A; 3 C; 4 G; 6 T; 0 OTHER.

Query Match 100.0%; Score 9; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.09e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TTCTCAGAA 9
|||||
Cp 9 ttctcagaa 1

RESULT 2
ID PCT-US97-20528-6 STANDARD; DNA; UNC; 32 BP.
AC xxxxxx
DT
DE Sequence 6, Application PC/TUS9720528
CC Sequence 6, Application PC/TUS9720528
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Improved Expression Vectors
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew LLP
CC STREET: Two Embarcadero Center, Eighth Floor
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94111-3834
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US97/20528
CC FILING DATE: Not yet assigned
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 60/029,545
CC FILING DATE: 08-NOV-1996
CC ATTORNEY/AGENT INFORMATION:

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4

CC NAME: Smith, Timothy L.
CC REGISTRATION NUMBER: 35,367
CC REFERENCE/DOCKET NUMBER: 014137-009610PC
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 576-0200
CC TELEFAX: (415) 576-0300
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 32 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA
SQ SEQUENCE 32 BP; 12 A; 8 C; 2 G; 10 T; 0 OTHER.

Query Match 100.0%; Score 9; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.09e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 15 TTCTCAGAA 23
|||||
Cp 9 ttctcagaa 1

RESULT 3
ID US-09-024-753-146 STANDARD; DNA; UNC; 33 BP.
AC xxxxxx
DT
DE Sequence 146, Application US/09024753
CC Sequence 146, Application US/09024753
CC GENERAL INFORMATION:
CC APPLICANT: Reed, Steven G.
CC APPLICANT: Skeiky, Yasir A.W.
CC APPLICANT: Dillon, Davin C.
CC APPLICANT: Campos-Neto, Antonia
CC APPLICANT: Houghton, Raymond
CC APPLICANT: Vedvick, Thomas S.
CC APPLICANT: Twardzik, Daniel R.
CC APPLICANT: Lodes, Michael J.
CC TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
CC NUMBER OF SEQUENCES: 236
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: SEED and BERRY LLP
CC STREET: 6300 Columbia Center, 701 Fifth Avenue
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98104-7092
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/09/024,753
CC FILING DATE: 18-FEB-1998
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Maki, David J.
CC REGISTRATION NUMBER: 31,392
CC REFERENCE/DOCKET NUMBER: 210121.417C8
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206) 622-4900
CC TELEFAX: (206) 682-6031

CC INFORMATION FOR SEQ ID NO: 146:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 33 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: other nucleic acid
CC DESCRIPTION: /desc = "PCR primer"
CC ORIGINAL SOURCE:
CC ORGANISM: Mycobacterium tuberculosis
SQ SEQUENCE 33 BP; 11 A; 7 C; 9 G; 6 T; 0 OTHER.

Query Match 100.0%; Score 9; DB 23; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.09e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 8 TTCTCAGAA 16
|||||
Cp 9 ttctcagaa 1

RESULT 4
ID US-08-997-522-3 STANDARD; DNA; UNC; 192 BP.
AC xxxxxx
DT
DE Sequence 3, Application US/08997522
CC Sequence 3, Application US/08997522
CC GENERAL INFORMATION:
CC APPLICANT: Rundell, Clark A.
CC APPLICANT: Vary, Calvin P.H.
CC TITLE OF INVENTION: STABLE ENCAPSULATED REFERENCE
CC TITLE OF INVENTION: NUCLEIC ACID AND METHOD OF MAKING
CC NUMBER OF SEQUENCES: 5
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: Wood, Herton & Evans, L.L.P.
CC STREET: 2700 Carew Tower
CC CITY: Cincinnati
CC STATE: OH
CC COUNTRY: USA
CC ZIP: 45202-2917
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FastSeq for Windows DEMONSTRATION Version 2.00
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/997,522
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/905,124
CC FILING DATE: 31-Jul-1997
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Frei, Donald F
CC REGISTRATION NUMBER: 21,190
CC REFERENCE/DOCKET NUMBER: CASI-02C1-107
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 513-241-2324
CC TELEFAX: 513-421-7269
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 3:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 192 base pairs
CC TYPE: nucleic acid

CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC ORIGINAL SOURCE:
CC ORGANISM: human
CC CELL TYPE: lymphocyte
SQ SEQUENCE 192 BP; 55 A; 39 C; 41 G; 57 T; 0 OTHER.

Query Match 100.0%; Score 9; DB 22; Length 192;
Best Local Similarity 100.0%; Pred. No. 4.09e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 TTCTCAGAA 111
|||||
Qy 1 ttctcagaa 9

RESULT 5
ID US-08-451-242A-762 STANDARD; DNA; UNC; 214 BP.
AC xxxxxx
DT
DE Sequence 762, Application US/08451242A
CC Sequence 762, Application US/08451242A
CC GENERAL INFORMATION:
CC APPLICANT: Seilhamer, Jeffrey J.
CC APPLICANT: Delegeane, Angelo M.
CC APPLICANT: Bille, Pamela Kay
CC APPLICANT: Pham, Mino Thu
CC APPLICANT: Altus, Christina M.
CC APPLICANT: Hillman, Jennifer L.
CC APPLICANT: Akerblom, Ingrid E.
CC TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED
CC TITLE OF INVENTION: FROM HUMAN TESTES
CC NUMBER OF SEQUENCES: 3626
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
CC STREET: 3174 PORTER DRIVE
CC CITY: PALO ALTO
CC STATE: CALIFORNIA
CC COUNTRY: USA
CC ZIP: 94304
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/451,242A
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: CERRONE, MICHAEL C., Ph.D.
CC REGISTRATION NUMBER: 39132
CC REFERENCE/DOCKET NUMBER: PD-0025 US
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 855-0555
CC TELEFAX: (415) 845-4166
CC INFORMATION FOR SEQ ID NO: 762:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 214 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear

CC MOLECULE TYPE: cDNA
CC IMMEDIATE SOURCE:
CC CLONE: 127044
SQ SEQUENCE 214 BP; 70 A; 43 C; 48 G; 49 T; 4 OTHER.

Query Match 100.0%; Score 9; DB 17; Length 214;
Best Local Similarity 100.0%; Pred. No. 4.09e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 26 TTCTCAGAA 34
|||||||
Cp 9 ttctcagaa 1

RESULT 6
ID US-08-221-623A-409 STANDARD; DNA; UNC; 221 BP.
AC xxxxxx
DT

DE Sequence 409, Application US/08221623A
CC Sequence 409, Application US/08221623A
CC GENERAL INFORMATION:
CC APPLICANT: Adams, Mark D., et. al.
CC TITLE OF INVENTION: Human Genes, Sequences, and Expression
CC TITLE OF INVENTION: Products
CC NUMBER OF SEQUENCES: 3319
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Carella, Byrne, Baln, Gilfillan, Cecchi, Stewart, &
CC STREET: 6 Becker Farm Road
CC CITY: Roseland
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 07068
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb storage
CC COMPUTER: HP Vectra 486/33
CC OPERATING SYSTEM: MSDOS version 5.0
CC SOFTWARE: ASCII Text
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/221, 623A
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Olstein, Elliot
CC REGISTRATION NUMBER: 24,025
CC REFERENCE/DOCKET NUMBER: 325800-73
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (201) 994-1100
CC TELEFAX: (201) 994-1744
CC INFORMATION FOR SEQ ID NO: 409:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 221 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
SQ SEQUENCE 221 BP; 86 A; 27 C; 56 G; 50 T; 2 OTHER.

Query Match 100.0%; Score 9; DB 14; Length 221;
Best Local Similarity 100.0%; Pred. No. 4.09e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 196 TTCTCAGAA 204
|||||||
Cp 1 ttctcagaa 9

RESULT 7
ID US-60-090-762-370 STANDARD; DNA; UNC; 221 BP.
AC xxxxxx
DT

DE Sequence 370, Application US/60090762
CC Sequence 370, Application US/60090762
CC GENERAL INFORMATION:
CC APPLICANT: Lal, Preeti
CC APPLICANT: Tang, Y. Tom
CC APPLICANT: Gorgone, Gina
CC APPLICANT: Corley, Neil C.
CC APPLICANT: Guebler, Karl J.
CC APPLICANT: Baughn, Mariah R.
CC TITLE OF INVENTION: SIGNAL PEPTIDE-CONTAINING MOLECULES
CC NUMBER OF SEQUENCES: 445
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
CC STREET: 3174 PORTER DRIVE
CC CITY: PALO ALTO
CC STATE: CALIFORNIA
CC COUNTRY: USA
CC ZIP: 94304
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/60/090,762
CC FILING DATE: Herewith
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: CERRONE, MICHAEL C.
CC REGISTRATION NUMBER: 39,132
CC REFERENCE/DOCKET NUMBER: PF-0541 P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (650) 855-0555
CC TELEFAX: (650) 845-4166
CC INFORMATION FOR SEQ ID NO: 370:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 221 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC IMMEDIATE SOURCE:
CC LIBRARY: CONN001
CC CLONE: 1957710F6
SQ SEQUENCE 221 BP; 54 A; 40 C; 57 G; 70 T; 0 OTHER.

Query Match 100.0%; Score 9; DB 27; Length 221;
Best Local Similarity 100.0%; Pred. No. 4.09e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 143 TTCTCAGAA 151
|||||||
Cp 9 ttctcagaa 1

RESULT 8

ID US-60-089-037-209 STANDARD; DNA; UNC; 255 BP.
AC xxxxxx
DT
DE Sequence 209, Application US/60089037
CC Sequence 209, Application US/60089037
CC GENERAL INFORMATION:
CC APPLICANT: Stuve, Laura L.
CC APPLICANT: Corley, Neil C.
CC APPLICANT: Garrow, Bonnie L.
CC TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM RAT
CC TITLE OF INVENTION: MEDULLA OBLONGATA
CC NUMBER OF SEQUENCES: 2700
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
CC STREET: 3174 PORTER DRIVE
CC CITY: PALO ALTO
CC STATE: CALIFORNIA
CC COUNTRY: USA
CC ZIP: 94304
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/60/089, 037
CC FILING DATE:
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: MOENZEN, COLETTED C.
CC REGISTRATION NUMBER: 39,784
CC REFERENCE/DOCKET NUMBER:
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (650) 855-0555
CC TELEFAX: (650) 845-4166
CC INFORMATION FOR SEQ ID NO: 209:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 255 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC IMMEDIATE SOURCE:
CC CLONE: 701026892H1
SQ SEQUENCE 255 BP; 80 A; 43 C; 63 G; 66 T; 3 OTHER.
Query Match 100.0%; Score 9; DB 10; Length 255;
Best Local Similarity 100.0%; Pred. No. 4.09e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 46 TTCTGAGAA 54
|||||||
Cp 9 ttctcagaa 1

RESULT 9
ID US-08-757-204-279 STANDARD; DNA; UNC; 269 BP.
AC xxxxxx
DT
DE Sequence 279, Application US/08757204
CC Sequence 279, Application US/08757204
CC GENERAL INFORMATION:
CC APPLICANT: Gooding, Douglas H.
CC APPLICANT: Stuve, Laura L.

CC APPLICANT: Stuart, Susan G.
CC APPLICANT: Ito, Laura Y.
CC APPLICANT: Akerblom, Ingrid E.
CC APPLICANT: Delegeane, Angelo M.
CC APPLICANT: Naughton, Rebecca E.
CC APPLICANT: Klingler, Tod M.
CC TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
CC TITLE OF INVENTION: HUMAN CEREBELLUM
CC NUMBER OF SEQUENCES: 3609
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
CC STREET: 3174 PORTER DRIVE
CC CITY: PALO ALTO
CC STATE: CALIFORNIA
CC COUNTRY: USA
CC ZIP: 94304
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/757, 204
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 60/007,720
CC FILING DATE: November 30, 1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 60/008,793
CC FILING DATE: DECEMBER 18, 1995
CC ATTORNEY/AGENT INFORMATION:
CC NAME: CERRONE, MICHAEL C.
CC REGISTRATION NUMBER: 39,132
CC REFERENCE/DOCKET NUMBER: PD-0089 US
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 855-0555
CC TELEFAX: (415) 845-4166
CC INFORMATION FOR SEQ ID NO: 279:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 269 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC IMMEDIATE SOURCE:
CC CLONE: 669450
SQ SEQUENCE 269 BP; 97 A; 41 C; 43 G; 87 T; 1 OTHER.
Query Match 100.0%; Score 9; DB 20; Length 269;
Best Local Similarity 100.0%; Pred. No. 4.09e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 80 TTCTGAGAA 88
|||||||
Cy 1 ttctcagaa 9

RESULT 10
ID US-60-089-805-3218 STANDARD; DNA; UNC; 284 BP.
AC xxxxxx
DT
DE Sequence 3218, Application US/60089805
CC Sequence 3218, Application US/60089805

CC GENERAL INFORMATION:
CC APPLICANT: Stuve, Laura L.
CC APPLICANT: Gooding, Douglas H.
CC APPLICANT: Ito, Laura Y.
CC APPLICANT: Sherman, Bradley K.
CC TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED
CC TITLE OF INVENTION: FROM CORN LEAF
CC NUMBER OF SEQUENCES: 6686
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Incyte Pharmaceuticals, Inc.
CC STREET: 3174 Porter Drive
CC CITY: Palo Alto
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94304
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: Word Perfect 6.1/MS-DOS 6.2 software
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/60/089, 805
CC FILING DATE: HEREWITH
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: CERRONE, MICHAEL M.
CC REGISTRATION NUMBER: 36,132
CC REFERENCE/DOCKET NUMBER: PL-0022 P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 650-855-0555
CC TELEFAX: 650-845-4166
CC INFORMATION FOR SEQ ID NO: 3218:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 284 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC IMMEDIATE SOURCE:
CC CLONE: 700427643H1
CC SEQUENCE 284 BP; 81 A; 58 C; 76 G; 67 T; 2 OTHER.
Query Match 100.0%; Score 9; DB 10; Length 284;
Best Local Similarity 100.0%; Pred. No. 4.09e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 221 TTCTCAGAA 229
|||||||
Cp 9 ttctcagaa 1

RESULT 11
ID US-60-090-170-1196 STANDARD; DNA; UNC; 291 BP.
AC xxxxxx
DT
DE Sequence 1196, Application US/60090170
CC Sequence 1196, Application US/60090170
CC GENERAL INFORMATION:
CC APPLICANT: Devlina Lahiri
CC APPLICANT: Chen Mu-Forster
CC APPLICANT: Jingdong Liu

CC TITLE OF INVENTION: Nucleic acid molecules and other molecules
CC TITLE OF INVENTION: associated with the Complex Carbohydrate synthesis and
CC TITLE OF INVENTION: Degradation Pathways
CC NUMBER OF SEQUENCES: 1555
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lawrence M. Lavin, Jr.
CC STREET: BB4F
CC STREET: Monsanto Company
CC STREET: 700 Chesterfield Parkway North
CC CITY: St. Louis
CC STATE: MO
CC COUNTRY: United States
CC ZIP: 63198
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette (3.5in, 1.44 MB)
CC COMPUTER: IBM PC/XT/AT, IBM PS/2 or compatibles
CC OPERATING SYSTEM: Windows 95/NT
CC SOFTWARE: WinZip 6.3
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/60/090,170
CC FILING DATE:
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lavin Jr., Lawrence M.
CC REGISTRATION NUMBER: 30,768
CC REFERENCE/DOCKET NUMBER: 04983.0021/38-21(15425)A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (314) 737-6670
CC TELEFAX: (314) 737-6047
CC INFORMATION FOR SEQ ID NO: 1196:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 291 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC HYPOTHETICAL: No
CC ANTI-SENSE: No
CC ORIGINAL SOURCE:
CC ORGANISM: Zea mays
CC DEVELOPMENTAL STAGE: undeveloped
CC TISSUE TYPE: leaf
CC IMMEDIATE SOURCE:
CC LIBRARY: SATMON011
CC CLONE: 700082188
CC SEQUENCE 291 BP; 79 A; 65 C; 52 G; 95 T; 0 OTHER.
Query Match 100.0%; Score 9; DB 27; Length 291;
Best Local Similarity 100.0%; Pred. No. 4.09e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 85 TTCTCAGAA 93
|||||||
Cp 9 ttctcagaa 1

RESULT 12
ID US-60-087-831-139 STANDARD; DNA; UNC; 293 BP.
AC xxxxxx
DT
DE Sequence 139, Application US/60087831
CC Sequence 139, Application US/60087831
CC GENERAL INFORMATION:
CC APPLICANT: Lalquidl, Raghnunath

CC APPLICANT: Ito, Laura Y.
CC APPLICANT: Sherman, Bradley
CC TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED
CC TITLE OF INVENTION: FROM CORN SEEDLING
CC NUMBER OF SEQUENCES: 3103
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Incyte Pharmaceuticals, Inc.
CC STREET: 3174 Porter Drive
CC CITY: Palo Alto
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94304
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: Word Perfect 6.1/MS-DOS 6.2 software
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/60/087, 831
CC FILING DATE: HEREMITH
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: CERRONE, MICHAEL M.
CC REGISTRATION NUMBER: 36,132
CC REFERENCE/DOCKET NUMBER: PL-0019 P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 650-855-0555
CC TELEFAX: 650-845-4166
CC INFORMATION FOR SEQ ID NO: 139:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 293 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC IMMEDIATE SOURCE:
CC CLONE: 700618953H1
SQ SEQUENCE 293 BP; 64 A; 83 C; 78 G; 68 T; 0 OTHER.
Query Match 100.0%; Score 9; DB 10; Length 293;
Best Local Similarity 100.0%; Pred. No. 4.09e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 154 TTCTGAGAA 162
|||
Qy 1 ttctgagaa 9

RESULT 13
ID US-09-041-720-1985 STANDARD; DNA; UNC; 305 BP.
AC xxxxxx
DE Sequence 1985, Application US/09041720
CC Sequence 1985, Application US/09041720
CC GENERAL INFORMATION:
CC APPLICANT: Gooding, Douglas H.
CC APPLICANT: Stuve, Laura L.
CC APPLICANT: Stuart, Susan G.
CC APPLICANT: Ito, Laura Y.
CC APPLICANT: Akerblom, Ingrid E.
CC APPLICANT: Delegeane, Angelo M.

CC APPLICANT: Naughton, Rebecca E.
CC APPLICANT: Klingler, Tod M.
CC TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
CC TITLE OF INVENTION: ADRENAL GLAND TUMOR
CC NUMBER OF SEQUENCES: 4388
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
CC STREET: 3174 PORTER DRIVE
CC CITY: PALO ALTO
CC STATE: CALIFORNIA
CC COUNTRY: USA
CC ZIP: 94304
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/09/041,720
CC FILING DATE: HEREMITH
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 60/040,197
CC FILING DATE: MARCH 14, 1997
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: CERRONE, MICHAEL C.
CC REGISTRATION NUMBER: 39,132
CC REFERENCE/DOCKET NUMBER: PD-0333 US
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (650) 855-0555
CC TELEFAX: (650) 845-4166
CC INFORMATION FOR SEQ ID NO: 1985:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 305 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC IMMEDIATE SOURCE:
CC CLONE: 2825143H1
SQ SEQUENCE 305 BP; 107 A; 51 C; 67 G; 79 T; 1 OTHER.

Query Match 100.0%; Score 9; DB 23; Length 305;
Best Local Similarity 100.0%; Pred. No. 4.09e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 76 TTCTGAGAA 84
|||
Qy 1 ttctgagaa 9

RESULT 14
ID US-08-451-242A-2503 STANDARD; DNA; UNC; 327 BP.
AC xxxxxx
DE Sequence 2503, Application US/08451242A
CC Sequence 2503, Application US/08451242A
CC GENERAL INFORMATION:
CC APPLICANT: Seilhamer, Jeffrey J.
CC APPLICANT: Delegeane, Angelo M.
CC APPLICANT: Bills, Pamela Kay
CC APPLICANT: Pham, Mino Thu
CC APPLICANT: Altue, Christina M.

CC APPLICANT: Hillman, Jennifer L.
CC APPLICANT: Akerman, Ingrid E.
CC TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED
CC TITLE OF INVENTION: FROM HUMAN TESTES
CC NUMBER OF SEQUENCES: 3626
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
CC STREET: 3174 PORTER DRIVE
CC CITY: PALO ALTO
CC STATE: CALIFORNIA
CC COUNTRY: USA
CC ZIP: 94304
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/451,242A
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: CERRONE, MICHAEL C., Ph.D.
CC REGISTRATION NUMBER: 39132
CC REFERENCE/DOCKET NUMBER: PD-0025 US
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 855-0555
CC TELEFAX: (415) 845-4166
CC INFORMATION FOR SEQ ID NO: 2503:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 327 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: 'cDNA
CC IMMEDIATE SOURCE:
CC CLONE: 276138
SQ SEQUENCE 327 BP; 87 A; 54 C; 65 G; 95 T; 26 OTHER.
Query Match 100.0%; Score 9; DB 17; Length 327;
Best Local Similarity 100.0%; Pred. No. 4.09e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 65 TTCTCAGAA 73
Cp 9 ttctcagaa 1

RESULT 15
ID US-60-090-762-369 STANDARD; DNA; UNC; 388 BP.
AC xxxxxx
DE Sequence 369, Application US/60090762
CC Sequence 369, Application US/60090762
CC GENERAL INFORMATION:
CC APPLICANT: Lal, Preeti
CC APPLICANT: Tang, Y. Tom
CC APPLICANT: Gorgone, Gina
CC APPLICANT: Corley, Neil C.
CC APPLICANT: Guegler, Karl J.
CC APPLICANT: Baughn, Mariah R.
CC TITLE OF INVENTION: SIGNAL PEPTIDE-CONTAINING MOLECULES
CC NUMBER OF SEQUENCES: 445
CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
CC STREET: 3174 PORTER DRIVE
CC CITY: PALO ALTO
CC STATE: CALIFORNIA
CC COUNTRY: USA
CC ZIP: 94304
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/60/090,762
CC FILING DATE: Herewith
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: CERRONE, MICHAEL C.
CC REGISTRATION NUMBER: 39,132
CC REFERENCE/DOCKET NUMBER: PF-0541 P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (650) 855-0555
CC TELEFAX: (650) 845-4166
CC INFORMATION FOR SEQ ID NO: 369:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 388 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC IMMEDIATE SOURCE:
CC LIBRARY: BRSTUT01
CC CLONE: 1920738R6
SQ SEQUENCE 388 BP; 98 A; 84 C; 108 G; 97 T; 1 OTHER.
Query Match 100.0%; Score 9; DB 27; Length 388;
Best Local Similarity 100.0%; Pred. No. 4.09e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 310 TTCTCAGAA 318
Cp 9 ttctcagaa 1

Search completed: Fri Jul 10 12:42:43 1998
Job time : 63 secs.

US08963288 (TM)

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MParch_mn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Jul 10 12:37:17 1998; MacPar time 62.08 Seconds

Tabular output not generated. 241.933 Million cell updates/sec

Title: >US08963288.SEQ

Description: (1-9) from us08963288.seq

Perfect Score: 9

N.A. Sequence: 1 ttctgagaa 9

Comp: aagactctt

Scoring table: TABLE default

Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 457396 seqs, 834335066 bases x 2

Post-Processing: Minimum Match 0%

Listing first 45 summaries

Database:

emb154

Database:

genbank106

13:gb_ba 14:gb_htg 15:gb_in 16:gb_om 17:gb_ov 18:gb_pat
19:gb_ph 20:gb_pl 21:gb_ptr 22:gb_ptr 23:gb_ro 24:gb_st
25:gb_sy 26:gb_un 27:gb_vl

Statistics: Mean 5.308; Variance 1.727; scale 3.074

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description	Pred. No.
1	9	100.0	256 16	BTU95976				Bos taurus microsatell	7.07e+03
2	9	100.0	343 21	MMAREP2				Rhesus monkey aliphoid	7.07e+03
3	9	100.0	651 21	HSRASP				Human Y18 mRNA for ras	7.07e+03
4	9	100.0	793 16	BOVCYT1				Bovine cytochrome p-45	7.07e+03
5	9	100.0	961 18	E08433				cDNA encoding L-chain	7.07e+03
6	9	100.0	1000 18	A07622				Amplified spliced mRNA	7.07e+03

7	9	100.0	1086 20	VIRRA57P				Vigna acoulifolia (Ra	7.07e+03
8	9	100.0	1140 16	DAU18873				Urens arctos GB04 mito	7.07e+03
9	9	100.0	1213 18	I01578				Sequence 10 from Paten	7.07e+03
10	9	100.0	1305 16	BTCONGL				B.taurus mRNA for cong	7.07e+03
11	9	100.0	1346 15	MSE22384				Manduca sexta mRNA for	7.07e+03
12	9	100.0	1555 13	CRTDAA				C.trachomatis 16S ribo	7.07e+03
13	9	100.0	1733 20	TKS18SR				T.mairei gene for 18S	7.07e+03
14	9	100.0	1850 22	D55696				Human mRNA for cystein	7.07e+03
15	9	100.0	1869 13	RBHSEN				Rhodospseudomonas virid	7.07e+03
16	9	100.0	2009 16	GOTBCAS01				Goat beta-casein gene,	7.07e+03
17	9	100.0	2147 22	D16815				Human RNA for FAR-1r,	7.07e+03
18	9	100.0	2187 21	HSU17473				Human calcitonin-like	7.07e+03
19	9	100.0	2258 18	A06977				H.sapiens mRNA for alb	7.07e+03
20	9	100.0	2323 15	BBO80KDC6A				Babesia bovis 80 kDa p	7.07e+03
21	9	100.0	3153 16	GOTRAL				C.hircus alpha-lactalb	7.07e+03
22	9	100.0	3893 16	CFU77716				Canis familiaris desmo	7.07e+03
23	9	100.0	4096 21	HSSSPN1AG				H.sapiens gene for spe	7.07e+03
24	9	100.0	4223 20	AIRTNAGIN				A.limmerus tRNA-Gln ge	7.07e+03
25	9	100.0	4269 20	AF042671				Arabidopsis thaliana f	7.07e+03
26	9	100.0	4969 18	I44531				Sequence 76 from paten	7.07e+03
27	9	100.0	5143 21	HSU24170				Human P21 (WAF1) gene,	7.07e+03
28	9	100.0	5891 17	AB001981				Pigeon DNA for alpha-D	7.07e+03
29	9	100.0	6895 16	BOVFACV2A				Bos taurus factor V va	7.07e+03
30	9	100.0	7336 18	A05160				Nucleotide sequence of	7.07e+03
31	9	100.0	9127 21	HUMHSD3BA				Human type II 3-beta h	7.07e+03
32	9	100.0	9692 13	PMTIMOPR				P.mirabilis (H14320) D	7.07e+03
33	9	100.0	10929 13	U67554				Methanococcus jannasch	7.07e+03
34	9	100.0	18808 16	BTF1UP1				B.taurus lactoferrin g	7.07e+03
35	9	100.0	23241 15	CEIM10D9				Caenorhabditis elegans	7.07e+03
36	9	100.0	30864 15	CET01H10				Caenorhabditis elegans	7.07e+03
37	9	100.0	34159 15	DMC16SH7				Drosophila melanogaste	7.07e+03
38	9	100.0	34256 15	CEIM10C8				Caenorhabditis elegans	7.07e+03
39	9	100.0	35506 22	HS24E5				Human DNA sequence fto	7.07e+03
40	9	100.0	36845 21	HDM1DS				Homo sapiens iduronate	7.07e+03
41	9	100.0	42361 15	CEC25D7				Caenorhabditis elegans	7.07e+03
42	9	100.0	86212 20	AB010074				Arabidopsis thaliana g	7.07e+03
43	9	100.0	106346 22	AC004045				Homo sapiens chromosom	7.07e+03
44	9	100.0	118654 14	AC004139				*** SEQUENCING IN PROG	7.07e+03
45	9	100.0	172048 22	HS179N16				Homo sapiens DNA seque	7.07e+03

ALIGNMENTS

RESULT	1	LOCUS	256 bp	DNA	MM	22-OCT-1997
DEFINITION	BTU95976	Bos taurus microsatellite DVEPC043, complete sequence.				
ACCESSION	U95976					
NID	g2555063					
KEYWORDS						
SOURCE	Bos taurus.					
ORGANISM	Bos taurus.					
REFERENCE	1	(bases 1 to 256)				
AUTHORS	Valman, D., Pailhoux, E., Schmitz, A., Giraud-Deville, C., Cotinot, C. and Criblin, E.P.					
TITLE	Mass production of genetic markers from a limited number of sorted chromosomes					
JOURNAL	Mamm. Genome 8 (2), 153-156 (1997)					
MEDLINE	97224587					
REFERENCE	2	(bases 1 to 256)				
AUTHORS	Criblin, E.P. and Valman, D.					
TITLE	Direct Submision					
JOURNAL	Submitted (01-APR-1997) Genetique Biochimique et Cytogenetique,					

INRA, Jouy-en-Josas 78352, France

FEATURES

source

1. .256

/organism="Bos taurus"

/note="microsatellite from sorted chromosomes"

/db_xref="taxon:9913"

/chromosome="X"

94. .111

/note="microsatellite DYPC043"

/rpt_type=tandem

/rpt_unit=TG

BASE COUNT 49 a 43 c 61 g 101 t 2 others

ORIGIN

Query Match 100.0%; Score 9; DB 16; Length 256;

Best Local Similarity 100.0%; Pred. No. 7.07e+03;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 210 TTCTGAGAA 218

|||||

1 ttctgagaa 9

RESULT 2

LOCUS MHARE2 343 bp DNA PRI 06-JUL-1989

DEFINITION Rhesus monkey aliphoid DNA repeat (pRh2 27).

ACCESSION X04006

NID 938082

KEYWORDS aliphoid repetitive sequence; repetitive sequence; tandem repeat.

SOURCE Rhesus monkey.

ORGANISM Macaca mulatta

Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.

REFERENCE 1 (bases 1 to 343)

AUTHORS Pike, L.M., Carlisle, A., Newell, C., Hong, S.B. and Musich, P.R.

TITLE Sequence and evolution of rhesus monkey aliphoid DNA

JOURNAL J. Mol. Evol. 23 (2), 127-137 (1986)

MEDLINE 86308057

COMMENT Data kindly reviewed (06-OCT-1986) by L. Pike.

FEATURES

source

1. .343

/organism="Macaca mulatta"

/db_xref="taxon:9544"

misc_feature 1. .343

/note="aliphoid DNA repeat"

BASE COUNT 104 a 62 c 73 g 104 t

ORIGIN

Query Match 100.0%; Score 9; DB 21; Length 343;

Best Local Similarity 100.0%; Pred. No. 7.07e+03;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 TTCTGAGAA 13

|||||

1 ttctgagaa 9

RESULT 3

LOCUS HSRASLP 651 bp RNA PRI 12-SEP-1993

DEFINITION Human Y18 mRNA for ras-like protein.

ACCESSION X53143

NID 935888

KEYWORDS GTP-binding protein; ras-like protein.

SOURCE human.

ORGANISM Homo sapiens

Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 651)

AUTHORS Drivas, G.

TITLE Direct Submission

JOURNAL Submitted (18-MAY-1990) Drivas G., Dept. of Biochemistry, New York University Medical Center, 550 First Avenue, New York, NY 10016, USA

REFERENCE 2 (bases 1 to 651)

AUTHORS Drivas, G.T., Shih, A., Coutavas, E.E., D'Eustachio, P. and Rush, M.G.

TITLE Identification and characterization of a human homolog of the Schizosaccharomyces pombe ras-like gene YPT-3

JOURNAL Oncogene 6 (1), 3-9 (1991)

MEDLINE 91125876

FEATURES

source

1. .651

/organism="Homo sapiens"

/db_xref="taxon:9606"

/cell_type="teratocarcinoma"

/cell_line="HTERA2"

/clone="Y18"

1. .651

/note="ras-like protein (AA 1-216)"

/codon_start=1

/db_xref="PID:935889"

/db_xref="SWISS-PROT:P24410"

/translation="MGTRDEYDYLEKVVLDSDSVGKSNLSRTPRNEPLESKSTI GVEFATRSIQVDEKTIKAQIMDTAGDERVRAITSAYRGAVGALLVDIAKILTYEV ERMKELRDHADSNIIVIMLVGKSDLSHRAVPTDEARAFASNGLSFIETSLDSTN VEAFFQTLITETIRIVSGKMSDRREDSPPNNVPIHPTTEKPKVCCQNI"

BASE COUNT 210 a 125 c 148 g 168 t

ORIGIN

Query Match 100.0%; Score 9; DB 21; Length 651;

Best Local Similarity 100.0%; Pred. No. 7.07e+03;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 528 TTCTGAGAA 536

|||||

9 ttctcagaa 1

RESULT 4

LOCUS BOVCYT1 793 bp DNA MAM 23-JAN-1992

DEFINITION Bovine cytochrome P-450 (11beta) gene, exon 1 and 5' end, clone lambdaDB11beta(7-1).

ACCESSION D00449

NID 9217539

KEYWORDS cytochrome; cytochrome P-450; steroid hormone.

SEGMENT 1 of 8

SOURCE Bovine adrenal DNA, clone lambdaDB11beta(7-1).

ORGANISM Bos taurus

Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 793)

AUTHORS Hashimoto, T., Morohashi, K. and Omura, T.

TITLE Cloning and characterization of bovine cytochrome P-450(11 beta) genes

JOURNAL J. Biochem. 105 (5), 676-679 (1989)

MEDLINE 89327182

FEATURES

Location/Qualifiers

source 1. .793
/organism="Bos taurus"
/db_xref="taxon:9913"
protein_bind 235. .244
/note="AP-2 binding site"
/bound_moiety="see note"
misc_signal 419. .426
/note="cAMP regulatory element"
TATA_signal 452. .457
/note="putative"
exon <490. .728
/note="cytochrome P-450 (11beta) gene, exon 1"
BASE COUNT 153 a 264 c 238 g 138 t
ORIGIN

Query Match 100.0%; Score 9; DB 16; Length 793;
Best Local Similarity 100.0%; Pred. No. 7.07e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 669 TTCTGAGAA 677
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1 ttctgagaa 9

RESULT 5
LOCUS E08433 961 bp DNA PAT 26-NOV-1996
DEFINITION cDNA encoding L-chain of anti-TMW-antibody.
ACCESSION E08433
NID 92176550
KEYWORDS JP 1994319396-A/6.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 961)
AUTHORS Yasuto,S., Toshihiko,K., Takaehi,K., Hitoaki,M., Maseaki,T. and
Maesaya,F.
TITLE PLANT FOR PRODUCTION ANTIVIRAL ANTICODY AND METHOD FOR CREATING THE
JOURNAL SAME PLANT
Patent: JP 1994319396-A 6 22-NOV-1994;
JAPAN TOBACCO INC, KURARAY CO LTD
COMMENT OS None
OC Artificial sequences.
PN JP 1994319396-A/6
PD 22-NOV-1994
PF 07-MAY-1993 JP 199331208
PI SAITO YASUTO, KOGIKU TOSHIHIKO, KAMISHIRO TAKASHI, PI
MURAFUJI HITOKI,
PI TAKAMI MASAOKI, FUMINO MASAAYASU
PC A01H5/00, C12N15/13, C12P21/08;
CC strandedness: Double;
CC topology: linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FH
FT source 1. .961
FT /organism="Artificial sequences" FT
FT misc_feature 1. .961
FT /note="cDNA encoding L-chain of FT
FT anti-TMW-antibody"
FT CDS 34. .753
FT /product="L-chain of anti-TMW-antibody" FT
FT 5'UTR 1. .33
FT 3'UTR 754. .961.

FEATURES
source 1. .961
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 243 a 255 c 213 g 250 t
ORIGIN

Query Match 100.0%; Score 9; DB 18; Length 961;
Best Local Similarity 100.0%; Pred. No. 7.07e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 26 TTCTGAGAA 34
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1 ttctgagaa 1

RESULT 6
LOCUS A07622 1000 bp RNA PAT 22-JUN-1993
DEFINITION Amplified spliced mRNA for HPV 16.
ACCESSION A07622
NID 9413120
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1000)
AUTHORS Cerutti,P., Whitcomb,J., Zijlstra,J. and De Villiers,E.M.
TITLE Detection of human papillomavirus DNA in cervix smears
JOURNAL Patent: EP 0373352-A 8 20-JUN-1990;
BEHRINGERKE Aktiengesellschaft
FEATURES
source 1. .1000
Location/Qualifiers
/organism="Artificial sequences"
BASE COUNT 340 a 170 c 231 g 259 t
ORIGIN

Query Match 100.0%; Score 9; DB 18; Length 1000;
Best Local Similarity 100.0%; Pred. No. 7.07e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 843 TTCTGAGAA 851
|||||
1 ttctgagaa 1

RESULT 7
LOCUS VIRB7P 1086 bp mRNA PLN 09-NOV-1993
DEFINITION Vigna aconitifolia (rab7p) mRNA, complete cds.
ACCESSION L14928
NID 9414841
KEYWORDS
SOURCE Vigna aconitifolia root nodule cDNA to mRNA.
ORGANISM Vigna aconitifolia
Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Rutanae; Sapindales; Fabaceae; Papilionoideae;
Vigna.
REFERENCE 1 (bases 1 to 1086)
AUTHORS Cheon,C.-I., Lee,N.-G., Siddique,A.-B., Bal,A.-K. and Verma,D.
TITLE Role of plant homologs of Rab1p and Rab7p in PBM biogenesis
JOURNAL EMBO J. 12, 4125-4135 (1993)
MEDLINE 94038894
FEATURES
source 1. .1086
Location/Qualifiers

/organism="Vigna aconitifolia"
/db_xref="taxon:3918"
/tissue_type="root module"
177. .797
/gene="Rab1p"
177. .797
/gene="Rab7p"
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/translation="MSLRRRTLLKVIYIGDTGKTSIMQYVHKFSQQTAKTIGAD
FYVKEIQLDRILVTLQHWDAQGERPSLGAVERADCVLAIDVNTMSPTLDNM
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EDFNDAFLCLIKAKAALNHEBDYIFQGIPEAAYENBQRSCAC"

BASE COUNT 305 a 209 c 253 g 319 t
ORIGIN

Query Match 100.0%; Score 9; DB 20; Length 1086;
Best Local Similarity 100.0%; Pred. No. 7.07e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 587 TTCTGAGAA 595
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Oy 1 ttctgagaa 9

RESULT 8
LOCUS UAU18873 1140 bp DNA MAM 06-DEC-1996
DEFINITION Ursus arctos GB04 mitochondrial cytochrome b (cyt b) gene, complete
cds.
ACCESSION 018873
NID 9882162
KEYWORDS
SOURCE brown bear.
ORGANISM Mitochondrion Ursus arctos
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
REFERENCE
AUTHORS Talbot, S.L. and Shields, G.F.
TITLE Phylogeography of brown bears (Ursus arctos) of Alaska and
paraphyly within the Ursidae
JOURNAL Mol. Phylogenet. Evol. 5 (3), 477-494 (1996)
MEDLINE 96364019
REFERENCE 2 (bases 1 to 1140)
AUTHORS Talbot, S.L.
TITLE Direct Submission
JOURNAL Submitted (19-DEC-1994) Sandra L. Talbot, Institute of Arctic
Biology, University of Alaska Fairbanks, Fairbanks, AK 99775-7000,
USA

FEATURES
source Location/Qualifiers
1. .1140
/organism="Ursus arctos"
/mitochondrion
/note="lineage GB04, 2 individuals"
/db_xref="taxon:9644"
/tissue_type="skeletal muscle"
1. .1140
/gene="cyt b"
1. .1140
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/db_xref="PID:9882163"
/transl_table=2
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ILTGFLAMHYTSDDTTAFSSVTHICRDVHGMVIRVANGASMEFTCLFMHVRGL
YGSYLESEETWNIIGILFTVMAATAFMGCVILQMGQNSFGCAVITNINLSAIPYIGTOL
VEMHWGFSVDKATLTFFRAHFHLPEPTILALAAVHLLFLHETGSNRPSCITSDDKI
PEHPYVITKIDILGALLTTALATVLESPDLGPDVYIPANPLSTPPHIREWYFLE
AVAILRISIPNKRIGCVALLFESLILALIPLLHSTSGQGMWFRPLSQCFLVLAVDLULT
LTMIGQPVPEHPFIIICQJLASILVFTLLVMPINAGIITENMLIKM"

BASE COUNT 327 a 338 c 166 g 309 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.07e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 325 TTCTCAGAA:333
|||||
Cp -9 ttctcagaa 1

RESULT 9
LOCUS 101578 1213 bp ss-DNA PAT 05-MAR-1993
DEFINITION Sequence 10 from Patent US 4915942.
ACCESSION 101578
NID 9271054
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1213)
AUTHORS Vergara, U., Ruiz, A., Ferreira, A., Nussenzweig, R. S. and
Nussenzweig, V. N.
TITLE Cross-reactive and protective epitopes of CS
JOURNAL Patent: US 4915942-A 10 10-APR-1990;
New York University;
New York, NY

FEATURES
source Location/Qualifiers
1. .1213
/organism="unknown"

BASE COUNT 351 a 288 c 337 g 237 t
ORIGIN

Query Match 100.0%; Score 9; DB 18; Length 1213;
Best Local Similarity 100.0%; Pred. No. 7.07e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 285 TTCTCAGAA 293
|||||
Cp 9 ttctcagaa 1

RESULT 10
LOCUS BTCONGL 1305 bp RNA MAM 28-JUL-1995
DEFINITION B. taurus mRNA for conglutinin.
ACCESSION X71774
NID 9395267
KEYWORDS conglutinin.
SOURCE cow.
ORGANISM Bos taurus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 1305)
AUTHORS Lu, J., Laureen, S. B., Thiel, S., Jensenius, J. C. and Reid, K. B.
TITLE The cDNA cloning of conglutinin and identification of liver as a
primary site of synthesis of conglutinin in members of the Bovidae

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/home/fuller/jul10/US08963288.SEQ.gz

9

JOURNAL Biochem. J. 292 (Pt 1), 157-162 (1993)
MEDLINE 93271452
REFERENCE 2 (bases 1 to 1305)
AUTHORS Reid, K.B.M.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1993) K.B.M. Reid, MRC Immunochimistry Unit,
University of Oxford, Dept of Biochemistry, South Parks Road,
Oxford OX1 30U, UK

FEATURES
source
1. 1305
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_id="Lambda gt11 bovine liver cDNA"
148. .207
148. .1263
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/db_xref="PID:g395268"
/db_xref="SMISS-PROT:P23805"
/translation="MLLPISVLLLTTPMRSIGADMTTSQKTIANACTLVWCSPLE
SGLPGLDGDGRCPEHGEKGPSPGAPGARGP GWVGP IGPKNQGVGEPPGKQDT
GRRGPPGMPGPARGREGSGKQSGMCPPTGPEKGTGKGVGAPEI0GPPGSGIKG
EKAPGCTGAPGAGVGTGSGAIGQGSAGRPGLGGRGDPGCTGAKGSGIAEA
NALKQRTYIIDGILRRFQNAFSQYKAVLFPDQAVGKXIFETAGAVKSYSDAVLCR
EAKGQLSPRSSAKENAVTQMTNADKNAIYSLNDISTEGKFTYTGELIVSNMADG
EPNNSDEQPEKVEIIFPDGKMDVPCSKQLLVICF"
208. .1260
mat_peptide
/product="congultinin"
BASE COUNT 322 a 340 c 405 g 238 t
ORIGIN

Query Match 100.0%; Score 9; DB 16; Length 1305;
Best Local Similarity 100.0%; Pred. No. 7.07e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 225 TTCTCAGAA 233
|||||
Cp 9 ttctcagaa 1

RESULT 11
LOCUS MSE223384 1346 bp mRNA INV 12-MAR-1998
DEFINITION Manduca sexta mRNA for 26S proteasome regulatory ATPase subunit 10b
(S10b).
ACCESSION AJ223384
NID 92960215
KEYWORDS ATPase.
SOURCE tobacco hornworm.
ORGANISM Manduca sexta
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Lepidoptera; Sphingioidea; Sphingidae; Manduca.
REFERENCE 1 (bases 1 to 1346)
AUTHORS Hastings, R.A., Dawson, S.P., Billett, M.A. and Mayer, R.J.
TITLE The regulatory ATPases S10b is not only present in the 26S
proteasome but also in a smaller 220 kDa complex and as free
molecules in the intersegmental muscles of the tobacco horn moth,
Manduca sexta

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1346)
AUTHORS Hastings, R.A.
TITLE Direct Submission
JOURNAL Submitted (12-JAN-1998) Hastings R.A., School of Biomedical
Sciences, University of Nottingham, Medical School, Queen's Medical
Centre, Nottingham, Notts, NG7 2UH, UK

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10

FEATURES
source
1. 1346
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/db_xref="taxon:7130"
90. .1280
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CDS
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/codon_start=1
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(S10b)"
/db_xref="PID:e1266343"
/db_xref="PID:g2960216"
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KQYKSENDLKAIGLVGQIVGEV/KQLTEERKTVKATNGPRVVGCRQDLKRLKGG
TRVALDMTTLTIMRHLPREVDPVLYNNSHEDPGVTTAAIGLAEQIRQLREYIELL
LNPFLFVRVGI1PPKCGCLLYGPGTGKTLIARAVASQDLANFLKAVSSAIVRKYIGSS
ARLIREMYVARDHQPCIIIFMDEIDALIGRRFSEGTSADEIORTLAEILNMGDFTS
LQVKYIIMATNRPDTPDPAIARGRIDRKIEIPIEPNQARLEIILKIHAP IAKHGEND
YEAVVKLSDTFNGADLNNVCTEAGLFAIRAREXYIIQEDLMKAVKVAADKRLKESKLD
YKPV"

BASE COUNT 402 a 311 c 349 g 284 t
ORIGIN

Query Match 100.0%; Score 9; DB 15; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.07e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 837 TTCTCAGAA 845
|||||
Cp 9 ttctcagaa 1

RESULT 12
LOCUS CHTDMA 1555 bp DNA BCT 27-FEB-1991
DEFINITION C.trachomatis 16S ribosomal RNA gene.
ACCESSION M59178
NID g144493
KEYWORDS 16S ribosomal RNA; ribosomal RNA small subunit.
SOURCE C.trachomatis (strain 434) DNA.
ORGANISM Chlamydia trachomatis
Eubacteria; Planctomycetales; Chlamydiales; Chlamydia.
REFERENCE 1 (bases 1 to 1555)
AUTHORS Weisburg, W.G., Hatch, T. and Moese, C.R.
JOURNAL Unpublished (1990)
FEATURES
source
1. 1555
/organism="Chlamydia trachomatis"
/db_xref="taxon:813"
BASE COUNT 401 a 324 c 472 g 358 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.07e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 TTCTCAGAA 13
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Cp 1 ttctcagaa 9

RESULT 13
LOCUS TXS185NR 1733 bp DNA PLN 17-FEB-1997
DEFINITION T.maltea gene for 18S ribosomal RNA.
ACCESSION D16445

NID 9442496
KEYWORDS 18S ribosomal RNA; 26S rRNA.
SOURCE Taxus mairei seedling leaves DNA, clones 2-7, 2-8, 2-9, 1-1, 1-5, 1-6.
ORGANISM Taxus mairei
Eukaryotae; mitochondrial eukaryotes; Viridiplantae; Charophyta/Embryophyta group; Embryophyta; vascular plants; seed plants; Coniferopsida; Coniferales; Taxaceae; Taxus.
REFERENCE 1 (bases 1 to 1733)
AUTHORS Chaw,S.M., Long,H., Wang,B.S., Zharkikh,A. and Li,W.H.
TITLE The phylogenetic position of Taxaceae based on 18S rRNA sequences
JOURNAL J. Mol. Evol. 37 (6), 624-630 (1993)
MEDLINE 94157935
REFERENCE 2 (sites)
AUTHORS Chaw,S.M., Sung,H.M., Long,H., Zharkikh,A. and Li,W.H.
TITLE The phylogenetic positions of the conifer genera Amentotaxus Phyllocladus, and Nageia inferred from 18S rRNA sequences
JOURNAL J. Mol. Evol. 41 (2), 224-230 (1995)
MEDLINE 95395878
REFERENCE 3 (sites)
AUTHORS Chaw,S.M., Zharkikh,A., Sung,H.M., Lau,T.C. and Li,W.H.
TITLE Molecular phylogeny of extant gymnosperms and seed plant evolution: analysis of nuclear 18S rRNA sequences
JOURNAL Mol. Biol. Evol. 14 (1), 56-68 (1997)
MEDLINE 97153823
REFERENCE 4 (bases 1 to 1733)
AUTHORS Chaw,S.-M.
TITLE Direct Submision
JOURNAL Submitted (11-JUN-1993) to the DDBJ/EMBL/GenBank databases. Shu-Miaw Chaw, Academia Sinica, Institute of Botany, #128, Yen-Chiu-Yuan Rd. sec.2, Taipei, Taiwan 11529, Republic of China (E-mail:bochow@ccvax.sinica.edu.tw, Tel:2-789-9590(ex.408), Fax:2-782-7954)
FEATURES
source Location/Qualifiers
1..1733
/organism="Taxus mairei"
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/cell_type="somatic"
/dev_stage="seedling"
/tissue_type="leaves"
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/gene="18S rDNA"
/note="ds PCR products"
/evidence="not experimental"
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BASE COUNT 425 a 388 c 475 g 445 t
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Best Local Similarity 100.0%; Pred. No. 7.07e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1049 TTCTGAGAA 1057
|||||
Qy 1 ttctgagaa 9
RESULT 14
LOCUS D55696 1850 bp mRNA PRI 14-MAR-1997
DEFINITION Human mRNA for cysteine protease, complete cds.
ACCESSION D55696
NID q1890049

KEYWORDS cysteine protease.
SOURCE Homo sapiens Adult Heart cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Euteria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (sites)
AUTHORS Tanaka,T., Inazawa,J. and Nakamura,Y.
TITLE Molecular cloning of a human cDNA encoding putative cysteine protease (PRSC1) and its chromosome assignment to 14q32.1
JOURNAL Cytogenet. Cell Genet. 74 (1-2), 120-123 (1996)
MEDLINE 97049087
REFERENCE 2 (bases 1 to 1850)
AUTHORS Tanaka,T., Inazawa,J. and Nakamura,Y.
TITLE Molecular cloning of a novel human cDNA encoding putative cysteine protease and its chromosomal assignment to 14q32.1 by fluorescence in situ hybridization
JOURNAL Unpublished (1995)
REFERENCE 3 (bases 1 to 1850)
AUTHORS Nakamura,Y.
TITLE Direct Submision
JOURNAL Submitted (18-JUN-1995) to the DDBJ/EMBL/GenBank databases. Yusuke Nakamura, Institute of Medical Science, The University of Tokyo, Laboratory of Molecular Medicine; 4-6-1 Sirokaneda, Minato-ku, Tokyo 108, Japan (E-mail:yusuke@ims.u-tokyo.ac.jp, Tel:03-5449-5372, Fax:03-5449-5433)
FEATURES
source Location/Qualifiers
1..1850
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
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/map="14q32.1"
/tissue_type="Heart"
46..1347
/EC_number="3.4.22"
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/db_xref="PID:d1010173"
/db_xref="PID:q1890050"
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1833..1838
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BASE COUNT 482 a 456 c 464 g 448 t
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Best Local Similarity 100.0%; Pred. No. 7.07e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1683 TTCTGAGAA 1691
|||||
Qy 1 ttctgagaa 9
RESULT 15
LOCUS RB1HSEN 1869 bp mRNA BCT 10-JAN-1997
DEFINITION Rhodopseudomonas viridis homospemidine synthase mRNA, complete

cds.

ACCESSION 177975
NID 92276406
KEYWORDS homopermidine synthase.
SOURCE Rhodopseudomonas viridis (library: DSM134) mRNA.
ORGANISM Blastochloris viridis
Blastochloris viridis
Eubacteria; Proteobacteria; alpha subdivision; Ancylobacter group;
Blastochloris.

REFERENCE 1 (bases 1 to 1869)
AUTHORS Tholl, D., Ober, D., Martin, M., Kellermann, J. and Hartmann, T.
TITLE Purification, molecular cloning and expression in Escherichia coli
of homopermidine synthase from Rhodopseudomonas viridis
JOURNAL Eur. J. Biochem. 240 (2), 373-379 (1996)
MEDLINE 96439066
COMMENT CSDB:S:76040

FEATURES
source Location/Qualifiers

5'UTR
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1..1869
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184..1617
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PKPFVFNVTMSVEGVSEGLQPAELGWTERTMPDNARGHDSGCCAGITLLQPGAN
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LHEMGSGKQSDMRILDETEIVDGIDELGVLLYHGKNVWYGSQLSIEETRLAPD
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LAQRPGLEPEDIDTSDPQPFQNVLVVD"

3'UTR
1618..1869
/partial
/note="putative"

BASE COUNT 299 a 648 c 620 g 302 t
ORIGIN

Query Match 100.0%; Score 9; DB 13; Length 1869;
Best Local Similarity 100.0%; Pred. No. 7.07e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1697 TTCTCAGAA 1705
|||||
Cp 9 ttctcagaa 1

NW50E6 (TM)

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MPerch_m n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Jul 10 12:40:30 1998; MasPar time 18.48 Seconds

Tabular output not generated. 62.033 Million cell updates/sec

Title: >US08963288.SEQ

Description: (1-9) from us08963288.seq

Perfect Score: 9

N.A. Sequence: 1 ttctgagaa 9

Comp: aagactctt

Scoring table: TABLE default

Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 176886 seqs, 63680241 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

n-genseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37

Statistics: Mean 4.217; Variance 1.817; scale 2.321

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description	Pred. No.
1	9	100.0	20	15	Q91527	ETS-2 Mapi RFLP prime	8.66e+02	
2	9	100.0	26	33	T84431	Interferon-beta gene	8.66e+02	
c	3	9	100.0	192	37	T96331	Subtelomeric 5a clone	8.66e+02
c	4	9	100.0	666	8	Q47358	Sequence encoding the	8.66e+02
c	5	9	100.0	673	37	T95699	Novel human gene, des	8.66e+02

c	6	9	100.0	918	8	Q47361	Sequence encoding fus	8.66e+02
c	7	9	100.0	960	1	Q03293	Recombinant DNA encod	8.66e+02
c	8	9	100.0	1047	37	T88112	Phenylalanine tRNA syn	8.66e+02
c	9	9	100.0	1092	37	T91592	Rat UBCE2A coding seq	8.66e+02
c	10	9	100.0	1129	37	V02237	Human MutT2 (hMutT2)	8.66e+02
c	11	9	100.0	1338	12	Q73130	Transactivating facto	8.66e+02
c	12	9	100.0	1625	33	T84538	Human kidney inward r	8.66e+02
c	13	9	100.0	2237	37	T90287	Human glycoposphatid	8.66e+02
c	14	9	100.0	2508	15	Q94018	Human 5HT transporter	8.66e+02
c	15	9	100.0	2533	16	Q93877	Human placental endot	8.66e+02
c	16	9	100.0	2675	31	T63340	Human host cell prote	8.66e+02
c	17	9	100.0	2756	4	Q26646	Encodes 5HT serotoni	8.66e+02
c	18	9	100.0	3000	15	Q92913	Human protein tyrosin	8.66e+02
c	19	9	100.0	3754	37	V01891	Human OTRK18 gene.	8.66e+02
c	20	9	100.0	3977	12	Q87699	Plasmod pD56/RSB11,S	8.66e+02
c	21	9	100.0	4035	1	Q05872	Sequence encoding hum	8.66e+02
c	22	9	100.0	4102	35	T85575	Human MSX receptor va	8.66e+02
c	23	9	100.0	4540	31	T69891	Human cyclin D1-human	8.66e+02
c	24	9	100.0	4626	35	T79498	Plasmod pBS13.	8.66e+02
c	25	9	100.0	4688	1	N92029	Sequence of recombina	8.66e+02
c	26	9	100.0	4977	10	Q44359	Plasmod pET8c123C5S.	8.66e+02
c	27	9	100.0	4977	10	Q44358	Plasmod pET8c-123.	8.66e+02
c	28	9	100.0	5042	37	T89493	Porcine heart-fatty a	8.66e+02
c	29	9	100.0	5056	37	T93749	Wild type human C3 pr	8.66e+02
c	30	9	100.0	5093	15	Q99876	KIP1 coding sequence.	8.66e+02
c	31	9	100.0	5120	37	V01426	Plasmod pCW-SmGST3 D	8.66e+02
c	32	9	100.0	5519	13	Q76040	Retrovirus vector pPO	8.66e+02
c	33	9	100.0	5528	13	Q76038	HCV GKS-33-BCD fusion	8.66e+02
c	34	9	100.0	5600	6	Q38251	pVE108.	8.66e+02
c	35	9	100.0	5620	4	Q27489	PAD-CW1 expression v	8.66e+02
c	36	9	100.0	6414	3	Q20733	Plasmod pBHA-1.	8.66e+02
c	37	9	100.0	7456	2	Q10686	Plasmod vector pAdCMV	8.66e+02
c	38	9	100.0	7507	14	Q91272	Hybrid activator vec	8.66e+02
c	39	9	100.0	7625	31	T71323	Tryptophan-2,3-dioxyg	8.66e+02
c	40	9	100.0	8841	14	Q89299	ATM open reading fram	8.66e+02
c	41	9	100.0	9171	37	T43497	cDNA encoding human B	8.66e+02
c	42	9	100.0	9354	37	T73164	Plasmod pTB113 used f	8.66e+02
c	43	9	100.0	9642	31	T71324	Intron 21 of human pr	8.66e+02
c	44	9	100.0	9837	37	T96851	Hereditary haemochrom	8.66e+02
c	45	9	100.0	10825	37	T96690		

ALIGNMENTS

RESULT 1
ID 091527 standard; DNA: 20 BP.
AC 091527;
DT 22-DEC-1995 (first entry)
DE ETS-2 Mapi RFLP primer.
KW Restriction fragment Length polymorphism; RFLP; point mutation;
KM mapping; primary; polymerase chain reaction; PCR; ETS-2; ss.
OS Synthetic.
PN CA2136705-A.
PD 27-MAY-1995.
PE 25-NOV-1994; 136705.
PR 26-NOV-1993; US-157269.
PA (CLAR-) CLARKE INST PSYCHIATRY.
PI Kennedy JL, Petronis A;
DR WPI; 93-253407/34.
PT Screening for polymorphism by amplification of pooled nucleic acid
PT - restriction with endonuclease(s), sepn. of fragments and
PT comparison of restriction patterns, for detecting disease related
PT mutation(s), in genetic mapping etc.
PS Example 5; Page 33; 48pp; English.

CC The primers given in 091526-27 were used for the analysis of
CC the ETS-2 MspI PCR-RFLP. Restriction patterns of PCR products
CC were compared to detect the polymorphism.

SQ Sequence 20 BP; 6 A; 2 C; 6 G; 6 T;

Query Match: ... 100.0%; Score 9; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.66e+02;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 ttctgagaa 19

|||||

Qy 1 ttctgagaa 9

RESULT 2

ID T84431 standard; DNA; 26 BP.

AC T84431;

DT 13-NOV-1997 (first entry)

DE Interferon-beta gene reverse primer for standard PCR.

KM KIT gene; pig; coat colour; pigmentation; primer; PCR;

KM polymerase chain reaction; interferon-beta; ss.

OS Synthetic.

PN M09105278-A1.

PD 13-FEB-1997.

PF 24-JUL-1996; G01794.

PR 12-DEC-1995; GB-025364.

PR 27-JUL-1995; GB-015385.

PA (DALC-) DALCERY PLC.

P1 Andersson L, Koller MJ, Plastow GS, Siggens KM;

P1 Males R;

DR WPI; 97-145712/13.

PT Determ. of coat colour genotype in pigs by analysis of the KIT gene

PT - for duplication or deletions, or analysis of KIT protein, used to

PT establish breeding programmes for pigs of selected colour

PS Claim 12; Page 39; 49pp; English.

CC Primers IFN-beta REVERSE (T84431) and IFN-beta CRC FORWARD (T84432)

CC are based on the pig interferon-beta (IFN-beta) gene. They can be

CC utilized in an internal standard PCR amplification of pig genomic

CC DNA, simultaneously with primers (see T84420-27) specific for the

CC pig KIT gene. DNA amplified from pig genomic DNA by the KIT gene

CC primers is quantitated by comparison to DNA amplified using the

CC IFN-beta primers. The 3 alleles for pig coat colour (I, inhibition

CC of coat colour; I(p), patch; and i, development of colour) can be

CC differentiated on the basis of duplication/deletion in the KIT gene.

CC This allows breeding of pigs with the desired, usually white, coat

CC colour.

SQ Sequence 26 BP; 6 A; 5 C; 6 G; 9 T;

Query Match: 100.0%; Score 9; DB 33; Length 26;

Best Local Similarity 100.0%; Pred. No. 8.66e+02;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 ttctgagaa 13

|||||

Qy 1 ttctgagaa 9

RESULT 3

ID T96331 standard; DNA; 192 BP.

AC T96331;

DT 08-APR-1998 (first entry)

DE Subclonemic 5a clone CST1024.

KM Detection; eukaryotic pathogen; subtelomeric; 5a clone;

KM telomerase activity; diagnosis; fungal infection; fungus; fungi;

KM material infection; malaria; ss.

OS Homo sapiens.

PN US5693932-A.

PD 09-DEC-1997.

PF 13-MAY-1993; 060952.

PR 13-MAY-1993; US-060952.

PR 13-MAY-1992; US-882438.

PR 24-MAR-1993; US-038766.

PA (RECC) UNIV CALIFORNIA.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Blackburn EH, McEachern MJ, Shay J, West MD, Wright W;

DR WPI; 98-041292/04.

PT Detection of eukaryotic pathogens, especially fungal or Plasmodium

PT spp. - by detecting telomerase activity

PS Example 19; Columns 87-88; 82pp; English.

CC The present sequence can be used in a novel method for detecting a

CC eukaryotic pathogen in a patient. The method comprises obtaining a

CC sample of somatic tissue or cells from the patient, determining if

CC telomerase activity is present and correlating this with the

CC presence of the pathogen. The method is useful for diagnosis of

CC fungal infections, especially a fungus of the genus Candida,

CC Kluyveromyces, Saccharomyces, Sporothrix, Coccidioides,

CC Histoplasma, Blastomyces, Paracoccidioides, Cryptococcus,

CC Aspergillus, Mucor or Rhizopus, or malarial infections, especially

CC Plasmodium vivax, P. ovale, P. malariae or P. falciparum.

SQ Sequence 192 BP; 58 A; 49 C; 33 G; 52 T;

Query Match: 100.0%; Score 9; DB 37; Length 192;

Best Local Similarity 100.0%; Pred. No. 8.66e+02;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 41 ttctcagaa 49

|||||

Cp 9 ttctcagaa 1

RESULT 4

ID Q47358 standard; DNA; 666 BP.

AC Q47358;

DT 04-FEB-1994 (first entry)

DE Sequence encoding the HA2 subunit of haemagglutinin (HA) of A/Udm.

KM Vaccine; influenza virus; haemagglutinin subunit; HA2; Influenza A;

KM Influenza virus.

OS Influenza virus.

PH Key Location/Qualifiers

FT cds 1..663

FT . /tag= a

PN M09315763-A.

PD 19-AUG-1993.

PF 18-FEB-1993; U01451.

PR 18-FEB-1992; US-837773.

PA (SMK) SMITHKLINE BEECHAM CORP.

PI Dillon SB, Scott M, Shatzman A;

DR WPI; 93-272565/34.

DR P-PADB; R38864.

PT Vaccine against influenza A and B - contg. haemagglutinin 2

PT sub-unit of virus, and conferring multi-strain immunity

PS Disclosure; Page 44; 99pp; English.

CC The protein of the invention is derived from the HA2 subunit of a

CC haemagglutinin (HA) protein, e.g., from a H3N2 subtype virus. Among

CC H3N2 subtype strains of influenza A include A/Udm and A/Victoria

CC viruses. The nucleic acid sequences of the HA2 portions of the A/

CC Udm (Q47358) and A/Victoria (Q47359) strains were compared with

CC the nucleic acid sequence of a H1N1 subtype virus, A/PR/8/34 (Q43760)

CC in order to generate a consensus sequence.
SQ Sequence 666 BP; 223 A; 117 C; 167 G; 159 T;

Query Match 100.0%; Score 9; DB 8; Length 666;
Best Local Similarity 100.0%; Pred. No. 8.66e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 208 ttctcagaa 216
|||||||
Cp 9 ttctcagaa 1

RESULT 5
ID T95699 standard; DNA; 673 BP.
AC T95699;
DT 23-APR-1998 (first entry)
DE Novel human gene, designated WMP3.
KM Peptide recognition unit; YAP WW domain binding protein; WBP-1; WBP-2;
KM WW domain; cell signalling; growth regulation; cytoskeleton organisation;
KM targeted drug screening; modulator; WW domain interaction; WMP3; ss.
OS Homo sapiens.
PN M09317223-A1.
PD 09-OCT-1997.
PF 03-APR-1997; U05547.
PR 03-APR-1996; A6-630916.
PA (CYTO-) CYTOGEN CORP.
PA (UNNC-) UNIV NORTH CAROLINA.
PI Fowles DM, Kay BK, Pirozzi G;
DR WPI; 97-503234/46.
DR P-PSDB; W36796.
PT Identifying cell signalling and growth regulatory polypeptides by
PT reaction with multivalent recognition complex - polypeptides are
PT useful in targeted drug selection
PS Claim 68; Fig 20; 220pp; English.
CC The present DNA sequence encodes a novel protein WMP3. The WMP3 gene was
CC identified and isolated from human bone marrow and brain cDNA libraries,
CC using peptides W38103-05. These peptide recognition units are based on
CC the sequences of WW domain binding domains of the YAP WW domain binding
CC proteins WBP-1 and WBP-2. The WW domain is a small functional domain
CC found in a large number of proteins from a variety of species including
CC humans, nematodes and yeast. Its name is derived from the observation
CC that two tryptophan residues, one in the amino terminal portion of the
CC WW domain and one in the carboxyl terminal portion, are conserved. Most
CC proteins containing WW domains have a function involving cell signalling
CC and growth regulation or the organisation of the cytoskeleton.
CC Polypeptides containing a WW domain are identified by treating a
CC multivalent recognition unit complex that has selective binding affinity
CC for a WW domain, with many polypeptides and identifying those with
CC selective affinity for the complex. Proteins containing WW domains are
CC used for targeted drug screening, i.e. to identify potential modulators
CC of specific WW domain interactions. The valency of the recognition unit
CC is important in determining specificity of interaction with WW domains.
CC In multivalent form specificity is relaxed, but not lost, so proteins
CC containing WW domains similar, but not identical, to the sequence of the
CC peptides' target WW can be detected, including new polypeptides.
SQ Sequence 673 BP; 199 A; 163 C; 170 G; 141 T;

Query Match 100.0%; Score 9; DB 37; Length 673;
Best Local Similarity 100.0%; Pred. No. 8.66e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 396 ttctcagaa 404
|||||||
Cp 9 ttctcagaa 1

RESULT 6
ID Q47361 standard; DNA; 918 BP.
AC Q47361;
DT 04-FEB-1994 (first entry)

DE Sequence encoding fusion protein NS1(1-81)H3NA2(1-221)
KM Vaccine; influenza virus; haemagglutinin subunit; HA2; influenza A;
KM ss.
OS Synthetic.
FH Key Location/Qualifiers
FT cds 1..918
FT /*tag= a

PN M09315763-A.
PD 19-AUG-1993.
PF 18-FEB-1993; U01451.
PR 18-FEB-1992; US-837773.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PI Dillon SB, Scott M, Shatzman A;
DR WPI; 93-272565/34.
DR P-PSDB; R38867
PT Vaccine against influenza A and B - contg. haemagglutinin 2
PT sub-unit of virus, and conferring multi-strain immunity
PS Claim 19; Page 52-53; 99pp; English.
CC Proteins of the invention are derived from the HA2 subunit of a
CC haemagglutinin (HA) protein, e.g., from a H3N2 subtype virus. Among
CC H3N2 subtype strains of influenza A include A/Udorn and A/Victoria
CC viruses. Examples are Aas 1-221 and 77-221 of a selected H3HA2
CC subunit. Fusion proteins are also claimed, which include a protein
CC derived from a H3N2 subtype virus fused in frame with, e.g., the
CC NS1 portion derived from a H1N1 subtype virus, A/PR/8/34 (Q47360).
CC The NS1 portion may comprise residues 1-42 or 1-81 of H1N1.
CC Alternatively, the HA2 fragment may be fused to a portion of the
CC NS1 peptide derived from a selected type A virus, e.g., an H3
CC subtype virus (H3HA2), or a type B (BHA2) virus. The preferred type
CC B influenza virus is human virus strain B/Jae/40. The
CC NS1(1-81)H3HA2(1-221) protein has a three-dimensional structure which
CC is substantially similar to that of the NS1(1-81)HA2(1-222) protein
CC derived from H1N1 subtype virus (C13). However, it only has 50%
CC homology with the AA sequence of C13 protein.
SQ Sequence 918 BP; 295 A; 176 C; 234 G; 213 T;

Query Match 100.0%; Score 9; DB 8; Length 918;
Best Local Similarity 100.0%; Pred. No. 8.66e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 463 ttctcagaa 471
|||||||
Cp 9 ttctcagaa 1

RESULT 7
ID Q03293 standard; DNA; 960 BP.
AC Q03293;
DT 03-AUG-1990 (first entry)
DE Recombinant DNA encoding human prolactin (HP)
KM Human prolactin (HP); plasmid pTP100; plasmid pDR720; plasmid pLP100.
OS Homo sapiens.
PN J02000445-A.
PD 05-JAN-1990.
PF 25-DEC-1987; 331244.
PR 25-DEC-1987; JP-331244, JP-315317.
PA (SHIK-) Shikishima Boseki K.
PI

DR WP1; 90-04/987/07.
 P-PSDB; R05231.
 PT Human prolactin producing recombinant DNA -
 PT In which promoter, Shine-Dalgarno sequence and translation
 PT Initiation codon are integrated
 PS Disclosure; Fig 1; 15pp; Japanese.
 CC Also new are bacteria (E. coli) expressing HP which contain it and the
 CC prodn. of HP by their culture. A promoter, Shine-Dalgarno (SD)
 CC sequence and translation initiation codon (TIC) are inserted, in
 CC order, upstream of the HP gene. The HP gene is isolated from pHP100, the
 CC promoter, SD sequence and TIC are obtd. from pHR720, and these are
 CC ligated with a synthetic DNA linker to produce plasmid pHP100. It allows
 CC large amts. of HP to be produced recombinantly.
 S0 Sequence 960 BP; 287 A; 246 C; 209 G; 218 T;
 Query Match 100.0%; Score 9; DB 1; Length 960;
 Best Local Similarity 100.0%; Pred. No. 8.66e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 778 ttctcgagaa 786
 |||||||||
 1
 Oy 1 ttctcgagaa 9
 RESULT 8
 ID T88112 standard; DNA; 1047 BP.
 AC T88112;
 DT 28-APR-1998 (first entry)
 DE Phenylalanyl tRNA synthetase alpha subunit encoding DNA.
 KM Phenylalanyl tRNA synthetase; phes protein; bacterial infection;
 KM meningitis; vaccine; antibacterial; immune response; ss.
 OS Streptococcus pneumoniae.
 FH Key Location/Qualifiers
 FT CDS 1..1047
 FT /tag= a
 FT /product= "phes alpha subunit"
 PN W09738722-A1.
 PD 23-OCT-1997.
 PF 18-APR-1997; U06876.
 PR 18-APR-1996; GB-007993.
 PA (SMK) SMITHKLINE BEECHAM CORP.
 PA (SMK) SMITHKLINE BEECHAM PLC.
 PI Lawlor EJ;
 DR WP1; 97-526215/48.
 P-PSDB; W27668.
 PT Polynucleotide encoding Streptococcus pneumoniae phenylalanyl tRNA
 PT synthetase alpha and beta subunits - useful to diagnose, treat or
 PT prevent bacterial infection, especially meningitis
 PS Claim 5; Page 45; 53pp; English.
 CC The present sequence encodes the alpha subunit of phenylalanyl tRNA
 CC synthetase (phes) from Streptococcus pneumoniae 0100993 (NCIMB 40794).
 CC The polynucleotide encoding phes can be used for the recombinant
 CC production of phes, which can be used to treat conditions requiring phes
 CC activity. Sequences antisense to the polynucleotide can be used to
 CC control phes expression. Phes, or phes expressing vectors can be used to
 CC induce an immune response, i.e. an antibody (Ab) and/or T cell response,
 CC against S. pneumoniae to protect against infection, or to screen for
 CC antagonists or agonists of the polynucleotide encoding phes or phes's
 CC activity, i.e. antibacterials. The antagonist, e.g. an anti-phes Ab, can
 CC be used to treat conditions requiring phes inhibition, e.g. an
 CC S. pneumoniae infection, particularly meningitis. A fragment of the
 CC polynucleotide encoding phes can be used as a probe to isolate full length
 CC or related sequences, or diagnose, e.g. by polymerase chain reaction,
 CC infection stage and type, including mutation and polymorphism detection.

CC Diagnosis may also be achieved by detecting phes overexpression,
 CC e.g. by immunoassay. The Ab can be used to treat infection, isolate or
 CC identify phes expressing clones, purify phes and as an immunoassay
 CC reagent. More generally, the products can prevent adhesion of bacteria
 CC to wounds and in dwelling devices, block phes protein mediated invasion
 CC of mammalian cells and block the normal progression of infection.
 S0 Sequence 1047 BP; 284 A; 221 C; 261 G; 281 T;
 Query Match 100.0%; Score 9; DB 37; Length 1047;
 Best Local Similarity 100.0%; Pred. No. 8.66e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1027 ttctcgagaa 1035
 |||||||||
 Cp 9 ttctcgagaa 1
 RESULT 9
 ID T91592 standard; cDNA; 1092 BP.
 AC T91592;
 DT 20-APR-1998 (first entry)
 DE Rat UBCE2A coding sequence.
 KM Ubiquitin conjugating enzyme; UBCE2A; rat; ubiquitin; cell proliferation;
 KM transcription factor E2A; inhibitor; proteasome inhibitor; ds.
 OS Rattus sp.
 FH Key Location/Qualifiers
 FT CDS 82..558
 FT /tag= a
 PN W09735961-A1.
 PD 02-OCT-1997.
 PF 28-MAR-1997; U05337.
 PR 28-MAR-1996; US-014388.
 PA (HARD) HARVARD COLLEGE.
 PI Haber EJ, Kho C, Lee M;
 DR WP1; 97-489625/45.
 P-PSDB; W32487.
 PT Mammalian UBCE2A catalyses covalent attachment of ubiquitin to E2A -
 PT inhibitors of which can be used to inhibit proliferation of cell
 PT that express transcription factor E2A
 PS Claim 7; Page 47; 69pp; English.
 CC This sequence represents the coding sequence for the rat UBCE2A
 CC (ubiquitin conjugating enzyme) of the invention. The encoded protein
 CC catalyses the covalent attachment of ubiquitin to E2A. An anti-UBCE2A
 CC antibody or a single stranded nucleic acid that is antisense to a portion
 CC of this sequence that reduces the level of UBCE2A biological activity in
 CC a cell can be used to inhibit the proliferation of a cell that expresses
 CC transcription factor E2A. The proliferation of a cell may also be
 CC inhibited by introducing a proteasome inhibitor into the cell or by
 CC introducing into the cell a mutant E2A that possesses the transcripition
 CC activator activity of wild type E2A but lacks the UBCE2A binding site or
 CC lacks at least 1 of the lysine residues which are ubiquitination sites on
 CC the wild type E2A.
 S0 Sequence 1092 BP; 286 A; 264 C; 259 G; 283 T;
 Query Match 100.0%; Score 9; DB 37; Length 1092;
 Best Local Similarity 100.0%; Pred. No. 8.66e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 935 ttctcgagaa 943
 |||||||||
 Cp 9 ttctcgagaa 1
 RESULT 10

ID V02237; standard; cDNA; 1129 BP.
AC V02237;
DT 02-APR-1998 (first entry)
DE Human MutT2 (hmutt2) protein encoding cDNA.
KW MutT2 protein; human; hmutt2; treatment; DNA replication; gene therapy;
KW abnormal cell growth; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 120..779
FT /*tag= a
FT /product= hmutt protein*
PN US5695980-A.
PD 09-DEC-1997.
PF 06-JUN-1995; 470261.
PR 06-JUN-1995; US-470261.
PR 15-NOV-1994; WO-013187.
PA (HUMA-) HUMAN GENOME SCI.
PI Kitzhess EF, Wei Y;
DR WPI: 98-041304/04.
DR P-P508; W31692.
PT DNA encoding human MutT protein - useful to prevent and treat
PT diseases associated with errors in DNA replication and abnormal cell
PT growth
PS Claim 14; Columns 21-22; 22pp; English.
CC This cDNA encodes a mature human MutT2 protein (hmutt2). This hmutt2 DNA
CC is useful to prevent and treat diseases associated with errors in DNA
CC replication and abnormal cell growth, for example a tumour or a cancer.
CC The polypeptide can be utilized for specifically hydrolysing oxidised
CC nucleoside triphosphates, in particular, 8-oxo-dGTP, to the corresponding
CC monophosphate to ensure high fidelity of DNA synthesis. Probes comprising
CC nucleic acid molecules of sufficient length to specifically hybridise to
CC hmutt2 sequences and antibodies against mutt are useful for diagnosing a
CC disease or a susceptibility to a disease. Abnormal cellular growth,
CC related to a mutation in hmutt2 nucleic acid sequences and the protein
CC encoded by such nucleic acid sequences can be detected by these probes.
CC Antagonists to such mutated hmutt2 polypeptides, can be used to inhibit
CC the action of such polypeptides, for example, in the treatment of
CC tumours. The hmutt2 protein can be produced recombinantly and can be used
CC for gene therapy.
SQ Sequence 1129 BP; 333 A; 244 C; 258 G; 294 T;

Query Match 100.0%; Score 9; DB 37; Length 1129;
Best Local Similarity 100.0%; Pred. No. 8.66e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 ttctcagaa 154
|||||||
Cp 9 ttctcagaa 1

RESULT 11
ID 073130 standard; cDNA; 1338 BP.
AC 073130;
DT 26-MAY-1995 (first entry)
DE Transactivating factor TAF-1.
KW Transactivating factor; TAF-1; transcription activator;
KW transgenic plant; gene expression; G-box motif; rab16 motif 1;
KW tobacco; ss.
OS Nicotiana tabacum cv. SR1.
FH Key Location/Qualifiers
FT cde 9..806
FT /*tag= a
PN US5362864-A.
PD 08-NOV-1994.

PF 06-FEB-1991; 651710.
PR 06-FEB-1991; US-651710.
PA (UTRQ) UNITV ROCKEFELLER.
PI Chua N;
DR WPI: 94-357424/44.
DR P-P508; R62822.
PT Isolated transactivating factor, TAF-1 and encoding DNA - useful
PT to increase gene expression in plants
PS Disclosure; Columns 25/26-27/28; 39pp; English.
CC Partial cDNA clone p5a, encoding a C-terminal portion of
CC transactivating factor TAF-1 was isolated from a tobacco cDNA
CC expression library. The truncated TAF-1 protein binds to rab16
CC motif 1 and the B-box motif, and can be used to modulate gene
CC expression in transgenic plants or cell cultures.
SQ Sequence 1338 BP; 421 A; 244 C; 333 G; 340 T;

Query Match 100.0%; Score 9; DB 12; Length 1338;
Best Local Similarity 100.0%; Pred. No. 8.66e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 395 ttctagaa 403
|||||||
Qy 1 ttctagaa 9

RESULT 12
ID T84538 standard; cDNA to mRNA; 1625 BP.
AC T84538;
DT 03-DEC-1997 (first entry)
DE Human kidney inward rectifier K channel 3 (KIRK-3) cDNA.
KW KIRK-3; kidney inward rectifier potassium ion channel; human; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cde 77..1204
FT /*tag= a
PN W09712974-A2.
PD 10-APR-1997.
PF 09-SEP-1996; U14134.
PR 15-SEP-1995; US-003839.
PA (PRAA) PHARMACIA & UPJOHN CO.
PI Bienkowski MJ;
DR WPI: 97-226218/20.
DR P-P508; W26369.
PT New DNA encoding new human kidney potassium ion channel - and
PT transformed cells, useful for screening for potassium channel
PT modulators
PS Claim 1; Page 19-20; 38pp; English.
CC This cDNA sequence codes for a claimed human ATP-dependent potassium
CC channel designated KIRK-3 (see W26369), or kidney inward rectifier K
CC channel 3. A Genbank search using human ROMK1 cDNA as query sequence
CC identified a related rat cDNA (accession no. X83858) designated
CC BIRK (brain inward rectifier K channel) 10. Primers (see T84539-
CC 40) were designed and used to amplify a 1.2 kb BIRK10 product. The
CC BIRK10 cDNA was used to screen a human kidney cDNA library, and 2
CC sets of cDNA fragments were identified and designated KIRK-2 (see
CC T84537) and KIRK-3. ROMK1 was renamed KIRK-1. The KIRK-3 gene is
CC on chromosome 21, and KIRK-3 is expressed in kidney, pancreas and
CC lung. Also claimed are vectors or plasmids containing KIRK-2 or
CC KIRK-3 DNA, and bacterial, mammalian or yeast cells containing such
CC plasmids. The transformed cells are used to screen for compounds
CC that modulate human kidney, ATP-gated or related, K-channel activity.
SQ Sequence 1625 BP; 444 A; 399 C; 367 G; 415 T;

Query Match 100.0%; Score 9; DB 33; Length 1625;

Best Local Similarity 100.0%; Pred. No. 8.66e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1111 ttctcagaa 1119
|||||
Qy 1 ttctcagaa 9

RESULT 13
ID T90287 standard; cDNA; 2237 BP.
AC T90287;
DT 14-APR-1998 (first entry)
DE Human glycoposphatidylinositol anchored DAF cDNA.
KM Human glycoposphatidylinositol; GPI; anchored DAF; surface;
KM homologous complement restriction factor; HCRF; medical apparatus;
KM medical dressing; surgical equipment; diagnostic kit; prevention;
KM purification device; reduction; complement activation; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 65..1387
FT sig_peptide 65..166 /*tag= a
FT mat_peptide 167..1384 /*tag= b
FT /*tag= c

PN W09135886-A1.
PD 02-OCT-1997.
PF 12-MAR-1997; G00684.
PR 31-OCT-1996; GB-022694.
PR 22-MAR-1996; GB-006073.
PR 28-MAR-1996; GB-006516.
PA (IMOT-) IMOTRAN LTD.
PI Watkine NJ;
DR WPI; 97-489571/45.
DR P-PSDB; W27483.
PT Surfaces which prevent or reduce complement activation - having
PT surface bound homologous complement restriction factor
PS Example 1; Fig 1; 50pp; English.
CC The present sequence encodes human glycoposphatidylinositol (GPI)
CC anchored DAF. GPI anchored DAF was used in the development of a
CC novel surface bound to a homologous complement restriction factor
CC (HCRF), where the surface is not a surface to which HCRF binds in
CC vivo. The surface can be used in medical apparatus (e.g.
CC extra-corporeal circulation systems, tubing, valves, membranes,
CC pumps, oxygenators, catheters, cannulas, fluid reservoirs or
CC prostheses), medical dressings, surgical equipment, diagnostic kits
CC (e.g. kits for determining whether a patient has an abnormality
CC which prevents the complement system from working normally or from
CC being properly regulated) and purification devices (e.g. for
CC purifying complement components). The surface can be used to reduce
CC or prevent activation of complement, and to reduce morbidity due to
CC complement activation.
SQ Sequence 2237 BP; 699 A; 456 C; 474 G; 608 T;

Query Match 100.0%; Score 9; DB 37; Length 2237;
Best Local Similarity 100.0%; Pred. No. 8.66e+02;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1000 ttctcagaa 1008
|||||
Cp 9 ttctcagaa 1

RESULT 14

ID Q94018 standard; cDNA; 2508 BP.
AC Q94018;
DT 02-DEC-1995 (first entry)
DE Human 5HT transporter (hSERT).
KM Serotonin transporter; 5-hydroxytryptamine; 5HT; noradrenaline; NA;
KM SERT; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 73..1962
FT /*tag= a

PN US5418162-A.
PD 23-MAY-1995.
PF 22-OCT-1991; 778231.
PR 22-OCT-1991; US-778231.
PR 14-OCT-1992; US-959943.
PA (UYD0-) UNIV DUKE.
PA (UYEM-) UNIV EMORY.
PI Blakely RD, Caron MG, Freneau RT;
DR WPI; 95-199742/26.
DR P-PSDB; R76074.

PT DNA encoding rat serotonin transporter - useful in the rational design of
PT drugs and for screening for RFLP associated with certain disorders
PS Claim 12; column 37-42; 27pp; English.
CC An oligo probe capable of hybridising to a DNA consisting of a
CC portion of Q94018 is claimed. Poly (A+) RNA purified from a
CC placental trophoblastic cell line is used to prepare a human
CC placental cDNA library. A synthetic oligo based on partial
CC human 5HT transporter candidates was used to screen the
CC library. Three hybridising clones were identified. Two of these
CC clones were found to be homologous to rSERT and to be
CC identical with each other except for the presence of distinct
CC deletions in each cDNA. A PCR approach was used to ligate in-frame
CC the two pieces possessed uniquely by the two cDNAs.
SQ Sequence 2508 BP; 572 A; 652 C; 631 G; 653 T;

Query Match 100.0%; Score 9; DB 15; Length 2508;
Best Local Similarity 100.0%; Pred. No. 8.66e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 ttctcagaa 101
|||||
Cp 9 ttctcagaa 1

RESULT 15
ID Q93877 standard; cDNA to mRNA; 2533 BP.
AC Q93877;
DT 24-JUN-1996 (first entry)
DE Human placental endothelin converting enzyme partial cDNA clone.
KM Endothelin converting enzyme; ECE; inhibitor; human; placenta;
KM transgenic animal; big endothelin; hypertension; kidney failure;
KM cardiac arrest; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 1..2112
FT /*tag= a
FT /*note= "partial ORF, does not include start codon"

PN W09514095-A1.
PD 26-MAY-1995.
PF 10-NOV-1994; E03706.
PR 16-NOV-1993; DE-339100.
PR 07-FEB-1994; DE-403665.
PR 12-APR-1994; DE-412372.
PA (BAD1) BASF AG.

PI Hillen H, Jacob E, Meyer T, Otter R;
PI Schmidt M, Seuberger H, Subkowski T, Kroeger B;
DR WPI; 95-200385/26.
DR P-PSDB; R76237.
PT Bovine and human endothelin converting enzymes and corresp. DNA -
PT useful for identifying and preparing ECE inhibitors which can reduce
PT levels of endothelin
PS Example 8; Page 46-50; 72pp; German.
CC A cDNA clone (see Q93877), coding for part of the endothelin
CC converting enzyme ECE-1, was identified by screening a human
CC placental cDNA library with a bovine ECE-1 probe.
SQ Sequence 2533 BP; 620 A; 745 C; 674 G; 494 T;

Query Match 100.0%; Score 9; DB 16; Length 2533;
Best Local Similarity 100.0%; Pred. No. 8.66e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2044 ttctcagaa 2052
|||||
Cp 9 ttctcagaa 1

Search completed: Fri Jul 10 12:40:55 1998
Job time : 25 secs.

MUSE (TM)

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MPerch_mn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Jul 10 12:41:13 1998; MasPar time 4.42 Seconds

109.142 Million cell updates/sec

Tabular output not generated.

Title: >US08963288.SEQ

Description: (1-9) from us08963288.seq

Perfect Score: 9

N.A. Sequence: 1 tttctgagaa 9

Comp: aagactctt

Scoring table: TABLE default

Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 104157 seqs, 26825796 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: n-issued

1:5_COMB 2: PCT9_COMB 3: backfiles

Statistics: Mean 4.008; Variance 1.624; scale 2.469

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description	Pred. No.
c 1	9	100.0	9	2	PCT-US95-1	Sequence 34, Applicat	2.48e+02	
c 2	9	100.0	54	1	US-08-390-	Sequence 1036, Applic	2.48e+02	
c 3	9	100.0	495	2	PCT-US93-1	Sequence 6, Applicatio	2.48e+02	
c 4	9	100.0	521	2	PCT-US92-1	Sequence 13, Applicati	2.48e+02	
c 5	9	100.0	666	2	PCT-US94-0	Sequence 1, Applicatio	2.48e+02	
c 6	9	100.0	875	2	5258283-1	Patent No. 5258283.	2.48e+02	
c 7	9	100.0	1106	1	US-08-041-	Sequence 6, Applicatio	2.48e+02	
c 8	9	100.0	1273	1	US-07-794-	Sequence 2, Applicatio	2.48e+02	
c 9	9	100.0	1653	3	5198359-9	Patent No. 5198359.	2.48e+02	
c 10	9	100.0	1656	3	5449756-9	Patent No. 5449756.	2.48e+02	
c 11	9	100.0	1656	3	5198359-5	Patent No. 5198359.	2.48e+02	

c 12	9	100.0	1673	2	PCT-US91-0	Sequence 4, Applicatio	2.48e+02
c 13	9	100.0	1749	3	5258283-8	Patent No. 5258283.	2.48e+02
c 14	9	100.0	1940	1	US-08-429-	Sequence 3, Applicatio	2.48e+02
c 15	9	100.0	2042	1	US-08-439-	Sequence 1, Applicatio	2.48e+02
c 16	9	100.0	2096	1	US-08-205-	Sequence 10, Applicati	2.48e+02
c 17	9	100.0	2096	1	US-08-278-	Sequence 10, Applicati	2.48e+02
c 18	9	100.0	2214	3	5258502-1	Patent No. 5258502.	2.48e+02
c 19	9	100.0	2229	3	5470718-1	Patent No. 5470718.	2.48e+02
c 20	9	100.0	2316	3	5258283-6	Patent No. 5258283.	2.48e+02
c 21	9	100.0	2400	3	5215909-13	Patent No. 5215909.	2.48e+02
c 22	9	100.0	2563	3	5422248-1	Patent No. 5422248.	2.48e+02
c 23	9	100.0	3018	3	5200183-1	Patent No. 5200183.	2.48e+02
c 24	9	100.0	3064	2	PCT-US92-1	Sequence 14, Applicati	2.48e+02
c 25	9	100.0	3332	1	US-08-038-	Sequence 2, Applicatio	2.48e+02
c 26	9	100.0	3343	3	5453363-2	Patent No. 5453363.	2.48e+02
c 27	9	100.0	3903	3	5202236-12	Patent No. 5202236.	2.48e+02
c 28	9	100.0	4032	1	US-08-126-	Sequence 8, Applicatio	2.48e+02
c 29	9	100.0	4035	3	5449756-1	Patent No. 5449756.	2.48e+02
c 30	9	100.0	4035	3	5198359-1	Patent No. 5198359.	2.48e+02
c 31	9	100.0	4383	3	5194600-3	Patent No. 5194600.	2.48e+02
c 32	9	100.0	4454	1	US-07-712-	Sequence 1, Applicatio	2.48e+02
c 33	9	100.0	4626	2	PCT-US93-0	Sequence 27, Applicati	2.48e+02
c 34	9	100.0	4626	1	US-08-306-	Sequence 22, Applicati	2.48e+02
c 35	9	100.0	4969	1	US-08-260-	Sequence 76, Applicati	2.48e+02
c 36	9	100.0	5104	3	5506344-1	Patent No. 5506344.	2.48e+02
c 37	9	100.0	5173	1	US-08-242-	Sequence 1, Applicatio	2.48e+02
c 38	9	100.0	5238	3	5453363-1	Patent No. 5453363.	2.48e+02
c 39	9	100.0	5437	1	US-07-661-	Sequence 1, Applicatio	2.48e+02
c 40	9	100.0	5653	1	US-08-235-	Sequence 1, Applicatio	2.48e+02
c 41	9	100.0	5677	1	US-07-623-	Sequence 4, Applicatio	2.48e+02
c 42	9	100.0	7218	1	US-08-232-	Sequence 14, Applicati	2.48e+02
c 43	9	100.0	7326	3	5304637-21	Patent No. 5304637.	2.48e+02
c 44	9	100.0	8224	3	5180808-1	Patent No. 5180808.	2.48e+02
c 45	9	100.0	8540	1	US-08-149-	Sequence 2, Applicatio	2.48e+02

ALIGNMENTS

RESULT 1
ID PCT-US95-17025-34 STANDARD; DNA; UNC; 9 BP.
AC xxxxxx
DE Sequence 34, Application PC/TUS9517025
CC Sequence 34, Application PC/TUS9517025
CC GENERAL INFORMATION:
CC APPLICANT: James E. Darnell, Jr.
CC APPLICANT: Zilong Wen
CC APPLICANT: Curt M. Horvath
CC APPLICANT: Zhong Zhong
CC TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
CC TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
CC NUMBER OF SEQUENCES: 39
CC CORRESPONDENCE ADDRESS:
CC ADDRESS: Klauber & Jackson
CC STREET: 411 Hackensack Avenue
CC CITY: Hackensack
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 07601
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/17025
CC FILING DATE: 28-DEC-1995
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/369,796
CC FILING DATE: 06-JAN-1995
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Jackson Esq., David A.
CC REGISTRATION NUMBER: 26,742
CC REFERENCE/DOCKET NUMBER: 600-1-116
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 201 487-5800
CC TELEFAX: 201 343-1684
CC TELEX: 133521
CC INFORMATION FOR SEQ ID NO: 34:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 9 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA synthetic probe
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
SQ SEQUENCE 9 BP; 3 A; 2 C; 1 G; 3 T; 0 OTHER.

Query Match 100.0%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2,48e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TTCTCAGAA 9
|||||
Cp 9 ttctcagaa 1

RESULT 2
ID US-08-390-850-1036 STANDARD; DNA; UNC; 54 BP.
AC xxxxxx
DE Sequence 1036, Application US/08390850
CC Sequence 1036, Application US/08390850
CC Patent No. 5612215
CC GENERAL INFORMATION:
CC APPLICANT: Draper, Kenneth G.
CC APPLICANT: Pavco, Pamela
CC APPLICANT: McSwigen, James
CC APPLICANT: Gustofson, John
CC APPLICANT: Stinchcomb, Dan T.
CC TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
CC TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
CC NUMBER OF SEQUENCES: 1151
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lyon & Lyon
CC STREET: 633 West Fifth Street
CC STREET: Suite 4700
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: U.S.A.
CC ZIP: 90071
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
CC MEDIUM TYPE: storage
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: IBM P.C. DOS 5.0

CC SOFTWARE: FastSeq Version 1.5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/390,850
CC FILING DATE: February 17, 1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/354,920
CC FILING DATE: December 13, 1994
CC APPLICATION NUMBER: 08/152,487
CC FILING DATE: No. 5612215ember 12, 1993
CC APPLICATION NUMBER: 07/989,848
CC FILING DATE: December 7, 1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Warburg, Richard
CC REGISTRATION NUMBER: 32,327
CC REFERENCE/DOCKET NUMBER: 211/084
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC TELEX: 67-3510
CC INFORMATION FOR SEQ ID NO: 1036:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 54 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
SQ SEQUENCE 54 BP; 18 A; 12 C; 12 G; 0 T; 12 OTHER.

Query Match 100.0%; Score 9; DB 1; Length 54;
Best Local Similarity 66.7%; Pred. No. 2,48e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 4 UUCUCAGAA 12
:::|||||
Cp 9 ttctcagaa 1

RESULT 3
ID PCT-US93-10443-6 STANDARD; DNA; UNC; 495 BP.
AC xxxxxx
DE Sequence 6, Application PC/TUS9310443
CC Sequence 6, Application PC/TUS9310443
CC GENERAL INFORMATION:
CC APPLICANT: David D. Moore
CC APPLICANT: Jae W. Lee
CC TITLE OF INVENTION: NUCLEAR HORMONE RECEPTOR-
CC TITLE OF INVENTION: INTERACTING POLYPEPTIDES AND
CC TITLE OF INVENTION: RELATED MOLECULES AND METHODS
CC NUMBER OF SEQUENCES: 30
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fish & Richardson
CC STREET: 225 Franklin Street
CC CITY: Boston
CC STATE: Massachusetts
CC COUNTRY: U.S.A.
CC ZIP: 02110-2804
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
CC COMPUTER: IBM PS/2 Model 502 or 55SX
CC OPERATING SYSTEM: MS-DOS (Version 5.0)
CC SOFTWARE: WordPerfect (Version 5.1)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/10443
CC FILING DATE:

CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/969,136
CC FILING DATE: October 30, 1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Paul T. Clark
CC REGISTRATION NUMBER: 30,162
CC REFERENCE/DOCKET NUMBER: 00786/099002
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (617) 542-5070
CC TELEFAX: (617) 542-8906
CC TELEX: 200154
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 495
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
SQ SEQUENCE 495 BP; 152 A; 130 C; 98 G; 114 T; 1 OTHER.

Query Match 100.0%; Score 9; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 2.48e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 410 TTCTCAGAA 418
|||||
Cp 9 ttctcagaa 1

RESULT 4
ID PCT-US92-11353-13 STANDARD; DNA; UNC; 521 BP.
AC xxxxxx
DT
DE Sequence 13, Application PC/TUS9211353
CC Sequence 13, Application PC/TUS9211353
CC GENERAL INFORMATION:
CC APPLICANT: O'Hara, Patrick J
CC APPLICANT: Grant, Francis J
CC APPLICANT: Sheppard, Paul O
CC TITLE OF INVENTION: NOVEL HUMAN TRANSGUTAMINASES
CC NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: Townsend and Townsend
CC STREET: One Market Plaza, Stewart Street Tower
CC CITY: San Francisco
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94105-1492
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/11353
CC FILING DATE: 19921230
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/816,284
CC FILING DATE: 31-DEC-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Parmelee, Steve W
CC REGISTRATION NUMBER: 31-990
CC REFERENCE/DOCKET NUMBER: 13952-13-1

CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 206-467-9600
CC TELEFAX: 206-623-6793
CC INFORMATION FOR SEQ ID NO: 13:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 521 base pairs
CC TYPE: NUCLEIC ACID
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC IMMEDIATE SOURCE:
CC CLONE: PTC562
SQ SEQUENCE 521 BP; 136 A; 125 C; 155 G; 105 T; 0 OTHER.

Query Match 100.0%; Score 9; DB 2; Length 521;
Best Local Similarity 100.0%; Pred. No. 2.48e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 349 TTCTCAGAA 357
|||||
Cp 9 ttctcagaa 1

RESULT 5
ID PCT-US94-01149-1 STANDARD; DNA; UNC; 666 BP.
AC xxxxxx
DT
DE Sequence 1, Application PC/TUS9401149
CC Sequence 1, Application PC/TUS9401149
CC GENERAL INFORMATION:
CC APPLICANT: Shatzman, Allan
CC APPLICANT: Scott, Miller
CC APPLICANT: Dillon, Susan B.
CC APPLICANT: Kane, James
CC TITLE OF INVENTION: Vaccinal Polypeptides
CC NUMBER OF SEQUENCES: 72
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: SmithKline Beecham Corporation - Corporate
CC ADDRESS: Patents
CC STREET: U.S. Mailcode UM2220 - 709 Swedeland Road
CC CITY: King of Prussia
CC STATE: Pennsylvania
CC COUNTRY: USA
CC ZIP: 19406-2799
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/01149
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 149,150
CC FILING DATE: 05-NOV-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 013,415
CC FILING DATE: 01-FEB-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 108,914
CC FILING DATE: 18-AUG-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 837,773
CC FILING DATE: 18-FEB-1992

CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 751,896
CC FILING DATE: 30-AUG-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 387,200
CC FILING DATE: 28-JUL-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 238,801
CC FILING DATE: 02-NOV-1988
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 645,732
CC FILING DATE: 30-AUG-1984
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Baumeister, Kirk
CC REGISTRATION NUMBER: 33,833
CC REFERENCE/DOCKET NUMBER: P50134 PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 215-270-5096
CC TELEFAX: 215-270-5090
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 666 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: unknown
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..663
SQ SEQUENCE 666 BP; 223 A; 117 C; 167 G; 159 T; 0 OTHER.

Query Match 100.0%; Score 9; DB 2; Length 666;
Best Local Similarity 100.0%; Pred. No. 2.48e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 208 TTCTCAGAA 216
|||||
Cp 9 ttctcagaa 1

RESULT 6
ID 5258283-1 STANDARD; DNA; UNC; 948 BP.
AC xxxxxx
DT 01-JAN-1900
DE Patent No. 5258283.
CC APPLICANT: FRAZIER, MARVIN E.; MALLAVIA, LOUIS P.; SAMUEL, JAMES E.; BACA, OSMALD G.
CC TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF COXIELLA BURNETII IN BIOLOGICAL FLUIDS
CC NUMBER OF SEQUENCES: 17
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/425,856
CC FILING DATE: 23-OCT-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 927,779
CC FILING DATE: 05-NOV-1986
CC APPLICATION NUMBER: 795,207
CC FILING DATE: 05-NOV-1985
CC SEQ ID NO: 1:
CC LENGTH: 875
SQ Sequence 948 BP; 259 A; 161 C; 172 G; 283 T; 73 other;
Query Match 100.0%; Score 9; DB 3; Length 875;

Best Local Similarity 100.0%; Pred. No. 2.48e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 364 TTCTCAGAA 372
|||||
Cp 9 ttctcagaa 1

RESULT 7
ID US-08-041-648-6 STANDARD; DNA; UNC; 1106 BP.
AC xxxxxx
DE Sequence 6, Application US/08041648
CC Sequence 6, Application US/08041648
CC Patent No. 5486463
CC GENERAL INFORMATION:
CC APPLICANT: Leislauer, Werner
CC APPLICANT: Lischer, Hansruedi
CC APPLICANT: St ber, Dietrich
CC TITLE OF INVENTION: TNF-MOTIFINS
CC NUMBER OF SEQUENCES: 17
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.
CC STREET: 340 Klingelard Street
CC CITY: Nutley
CC STATE: New Jersey
CC COUNTRY: U.S.A.
CC ZIP: 07110-1199
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/041,648
CC FILING DATE: 1-APR-1993
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: EP 92810249.0
CC FILING DATE: 2-APR-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Roseman, Catherine R.
CC REGISTRATION NUMBER: 34240
CC REFERENCE/DOCKET NUMBER: RAN 4105/147
CC TELEPHONE: (201) 235-6208
CC TELEFAX: (201) 235-3500
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1106 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC FRAGMENT TYPE: N-terminal
CC ORIGINAL SOURCE:
CC ORGANISM: Plasmid pDS56/RBSII, SphI-TNFalpha(Se29)
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 994..1104
SQ SEQUENCE 1106 BP; 305 A; 258 C; 246 G; 297 T; 0 OTHER.

Query Match 100.0%; Score 9; DB 1; Length 1106;
Best Local Similarity 100.0%; Pred. No. 2,48e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 379 TTCTCAGAA 387
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0y 1 ttctcagaa 9

RESULT 8
ID US-07-794-731A-2 STANDARD; DNA; UNC; 1273 BP.
AC xxxxxx
DE Sequence 2, Application US/07794731A
CC Sequence 2, Application US/07794731A
CC Patent No. 5348867
CC GENERAL INFORMATION:
CC APPLICANT: George Georgiou
CC APPLICANT: Joseph A. Francisco
CC APPLICANT: Charles F. Earhart
CC TITLE OF INVENTION: Expression of Proteins on Bacterial
CC TITLE OF INVENTION: Surface
CC NUMBER OF SEQUENCES: 2
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Arnold, White & Durkee
CC STREET: P.O. Box 4433
CC CITY: Houston
CC STATE: Texas
CC COUNTRY: USA
CC ZIP: 77210
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy Disk
CC COMPUTER: IBM PC Compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Mordirect 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/794, 731A
CC FILING DATE: 19911115
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Kitchell, Barbara S.
CC REGISTRATION NUMBER: 33,928
CC REFERENCE/DOCKET NUMBER: GEOG:001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (512) 320-7200
CC TELEFAX: (512) 474-7577
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1273 base pairs
CC TYPE: NUCLEIC ACID
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC SEQUENCE 1273 BP; 339 A; 308 C; 332 G; 294 T; 0 OTHER.

Query Match 100.0%; Score 9; DB 1; Length 1273;
Best Local Similarity 100.0%; Pred. No. 2,48e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 663 TTCTCAGAA 671
|||||
Cp 9 ttctcagaa 1

RESULT 9

ID 5198359-9 STANDARD; DNA; UNC; 1791 BP.
AC xxxxxx
DT 01-JAN-1900
DE Patent No. 5198359
CC Patent No. 5198359
CC APPLICANT: TANIGUCHI, TADATSUGU;JATANEYAMA, MASANORI;
CC MINAMOTO, SEIJIRO;KONO, TAKESHI;DOI, TAKESHI;MIYASAKA, MASAYUKI;
CC TSUDO, MITSURU;KARASUYAMA, HAJIME
CC TITLE OF INVENTION: RECOMBINANT PROTEIN RECEPTOR FOR IL-2
CC NUMBER OF SEQUENCES: 9
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/487,059
CC FILING DATE: 05-MAR-1990
CC SEQ ID NO:9;
CC LENGTH: 1653
CC SEQUENCE 1791 BP; 316 A; 560 C; 455 G; 322 T; 138 other;

Query Match 100.0%; Score 9; DB 3; Length 1653;
Best Local Similarity 100.0%; Pred. No. 2,48e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 279 TTCTCAGAA 287
|||||
Cp 9 ttctcagaa 1

RESULT 10
ID 5449756-9 STANDARD; DNA; UNC; 1794 BP.
AC xxxxxx
DT 01-JAN-1900
DE Patent No. 5449756
CC Patent No. 5449756
CC APPLICANT: TANIGUCHI, TADATSUGU;HATAKEYAMA, MASANORI;MINAMOTO,
CC SEIJIRO;KONO, TAKESHI;DOI, TAKESHI;MIYASAKA, MASAYUKI;TSUDO,
CC MITSURU;KARASUYAMA, HAJIME
CC TITLE OF INVENTION: RECOMBINANT PROTEIN RECEPTOR FOR IL-2
CC NUMBER OF SEQUENCES: 12
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/88,592
CC FILING DATE: 9-JUL-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 865,155
CC FILING DATE: 08-APR-1992
CC APPLICATION NUMBER: 487,059
CC FILING DATE: 05-MAR-1990
CC SEQ ID NO:9;
CC LENGTH: 1656
CC SEQUENCE 1794 BP; 317 A; 559 C; 456 G; 324 T; 138 other;

Query Match 100.0%; Score 9; DB 3; Length 1656;
Best Local Similarity 100.0%; Pred. No. 2,48e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 282 TTCTCAGAA 290
|||||
Cp 9 ttctcagaa 1

RESULT 11
ID 5198359-5 STANDARD; DNA; UNC; 1794 BP.
AC xxxxxx
DT 01-JAN-1900
DE Patent No. 5198359
CC Patent No. 5198359

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/home/fuller/jul1898/US08963288_SEQ.rmi

11

```
CC APPLICANT: TANIGUCHI, TADATSUGO;ATAKEYAMA, MASANOBI;
CC MINAMOTO, SEJIRO;KONO, TAKESHI;DOI, TAKESHI;MIYASAKA, MASAYUKI;
CC TSUDO, MITSURU;KARASUYMA, HAJIME
CC TITLE OF INVENTION: RECOMBINANT PROTEIN RECEPTOR FOR IL-2
CC NUMBER OF SEQUENCES: 9
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/487, 059
CC FILING DATE: 05-MAR-1990
CC SEQ ID NO:5:
CC LENGTH: 1656
CC Sequence 1794 BP; 317 A; 560 C; 456 G; 323 T; 138 other;
CC Query Match 100.0%; Score 9; DB 3; Length 1656;
CC Best Local Similarity 100.0%; Pred. No. 2.48e+02;
CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cc 282 TTCTCAGAA 290
Cc |||||||||
Cc 9 ttctcagaa 1
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RESULT 12
ID PCT-US91-06148A-4 STANDARD; DNA; UNC; 1673 BP.
AC xxxxxx
DE Sequence 4, Application PC/TUS9106148A
CC Sequence 4, Application PC/TUS9106148A
CC GENERAL INFORMATION:
CC APPLICANT: Barry, Gerard F.
CC APPLICANT: Kishore, Ganesh M.
CC APPLICANT: Padgett, Stephen R.
CC TITLE OF INVENTION: Glycosate Tolerant
CC TITLE OF INVENTION: 5-Ethylpyruvylshikimate-3-Phosphate Synthases
CC NUMBER OF SEQUENCES: 36
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF
CC STREET: 700 Chesterfield Village Parkway
CC CITY: St. Louis
CC STATE: Missouri
CC COUNTRY: USA
CC ZIP: 63198
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US91/06148A
CC FILING DATE: 19910828
CC CLASSIFICATION: 800
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/07/749, 611
CC FILING DATE: 28-AUG-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/576, 537
CC FILING DATE: 31-AUG-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hoerner Jr., Dennis R.
CC REGISTRATION NUMBER: 30,914
CC REFERENCE/DOCKET NUMBER: 38-21(10535)
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (314)537-6099
CC TELEFAX: (314)537-6047
CC INFORMATION FOR SEQ ID NO: 4:
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Jul 10 12:37

/home/fuller/jul1898/US08963288_SEQ.rmi

12

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CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1673 base pairs
CC TYPE: NUCLEIC ACID
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 86..1432
CC SEQUENCE 1673 BP; 354 A; 517 C; 485 G; 317 T; 0 OTHER.
CC Query Match 100.0%; Score 9; DB 2; Length 1673;
CC Best Local Similarity 100.0%; Pred. No. 2.48e+02;
CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1653 TTCTCAGAA 1661
Db |||||||||
Db 1 ttctcagaa 9
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RESULT 13
ID 5258283-8 STANDARD; DNA; UNC; 1894 BP.
AC xxxxxx
DE 01-JAN-1900
DE Patent No. 5258283.
CC Patent No. 5258283
CC APPLICANT: FRAZIER, MARVIN E.;MALLAVIA, LOUIS P.;SAMUEL,
CC JAMES E.;BACA, OSWALD G.
CC TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF COXIELLA
CC BURNETTI IN BIOLOGICAL FLUIDS
CC NUMBER OF SEQUENCES: 17
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/425, 856
CC FILING DATE: 23-OCT-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 927,779
CC FILING DATE: 05-NOV-1986
CC APPLICATION NUMBER: 795,207
CC FILING DATE: 05-NOV-1985
CC SEQ ID NO:8:
CC LENGTH: 1749
CC Sequence 1894 BP; 579 A; 335 C; 343 G; 492 T; 145 other;
CC Query Match 100.0%; Score 9; DB 3; Length 1749;
CC Best Local Similarity 100.0%; Pred. No. 2.48e+02;
CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 807 TTCTCAGAA 815
Db |||||||||
Cc 9 ttctcagaa 1
```

```
RESULT 14
ID US-08-429-742-3 STANDARD; DNA; UNC; 1940 BP.
AC xxxxxx
DE Sequence 3, Application US/08429742
DE Sequence 3, Application US/08429742
CC Patent No. 5686257
CC GENERAL INFORMATION:
CC APPLICANT: Kennedy, Jacqueline
CC APPLICANT: Baran, J. Fernando
CC APPLICANT: Zlotnik, Albert
CC TITLE OF INVENTION: PURIFIED MAMMALIAN T CELL ANTIGENS AND
```

CC TITLE OF INVENTION: RELATED REAGENTS
CC NUMBER OF SEQUENCES: 4
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: DNA Research Institute
CC STREET: 901 California Avenue
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94304-1104
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/429,742
CC FILING DATE: 26-APR-1995
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Ching, Edwin P.
CC REGISTRATION NUMBER: 34,090
CC REFERENCE/DOCKET NUMBER: DX0505
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-852-9196
CC TELEFAX: 415-496-1200
CC INFORMATION FOR SEQ ID NO: 3:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1940 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 31..1197
CC SEQUENCE 1940 BP; 576 A; 464 C; 470 G; 430 T; 0 OTHER.
SQ
Query Match 100.0%; Score 9; DB 1; Length 1940;
Best Local Similarity 100.0%; Pred. No. 2.48e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 404 TTCTCAGAA 412
|||||
Cp 9 ttctcagaa 1

RESULT 15
ID US-08-439-145-1 STANDARD; DNA; UNC; 2042 BP.
AC xxxxxx
DT
Sequence 1, Application US/08439145
Sequence 1, Application US/08439145
Patent No. 5612472
GENERAL INFORMATION:
CC APPLICANT: Wilson, Stacy L.
CC APPLICANT: Brunke, Karen J.
CC TITLE OF INVENTION: NOVEL PLANT PROMOTER
CC NUMBER OF SEQUENCES: 1
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Sandoz Agro, Inc.
CC STREET: 975 California Avenue
CC CITY: Palo Alto
CC STATE: CA
CC COUNTRY: USA

CC ZIP: 94304
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/439,145
CC FILING DATE:
CC CLASSIFICATION: 800
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/075,690
CC FILING DATE:
CC APPLICATION NUMBER: US 07/791,929
CC FILING DATE: 09-JAN-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: No. 56124721s, Allen E.
CC REGISTRATION NUMBER: 34,490
CC REFERENCE/DOCKET NUMBER: 135-1082/CIP
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 354-3592
CC TELEFAX: (415) 857-1125
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 2042 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC SEQUENCE 2042 BP; 701 A; 363 C; 366 G; 612 T; 0 OTHER.
SQ
Query Match 100.0%; Score 9; DB 1; Length 2042;
Best Local Similarity 100.0%; Pred. No. 2.48e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 529 TTCTCAGAA 537
|||||
Cp 9 ttctcagaa 1

Search completed: Fri Jul 10 12:41:21 1998
Job time : 8 secs.

Release 3.1A John F. Collins, Biocomputing Research Unit
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Jul 10 12:38:49 1998; MasPar time 71.44 Seconds

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Percent Covered:	0

N.A. Sequence: 1 ttctgagaa 5

Comp:

Scoring table: TABLE default

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Post-processing: Minimum Match 0%

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Database: genbank-est106

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8:gb_est14 9:gb_est15 10:gb_est16 11:gb_est17

12:gb_est18 13:gb_est19 14:gb_est2 15:gb_est2

16:gb_est21 17:gb_est22 18:gb_est3 19:gb_est4

21:gb_est6 22:gb_est7 23:gb_est8 24:gb_est9 2

26:qb_sts

Statistics: Mean 5.477; Variance 0.789; scale 6.942

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	length	ID	Description	Pred. No.
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c	2	9	100.0	224	5	AA358477	1.22e+03
						E5779880 Plicenta 1 Ho	
c	3	9	100.0	241	6	H035066058	1.22e+03
						Human placenta cDNA 5'	
c	4	9	100.0	250	15	AA831260	1.22e+03
						oc731070.sl NCI C6AP GC	

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5	c	100.0	273.6	C03864	Human testis cDNA, clone	1.122e+03
6	c	100.0	279.20	ATTS5574	A. thaliana transcribe	1.122e+03
7	c	100.0	289.3	T06862	EST04751 Homo sapiens	1.122e+03
8	c	100.0	300.3	R01843	ye84a10.61 Homo sapien	1.122e+03
9	c	100.0	311.4	AA365753	EST76867 Pineal gland	1.122e+03
10	c	100.0	314.4	AA345536	EST51263 Gall bladder	1.122e+03
11	c	100.0	321.5	AA411400	zv28f01.61 Soares ovar	1.122e+03
12	c	100.0	324.14	R75614	y121g08.61 Homo sapien	1.122e+03
13	c	100.0	325.19	H88997	ye26b03.61 Homo sapien	1.122e+03
14	c	100.0	360.10	C60411	C.elegans cDNA clone y	1.122e+03
15	c	100.0	360.6	CEIK07405F	C.elegans cDNA clone y	1.122e+03
16	c	100.3	360.6	CEIK0826ZF	C.elegans cDNA clone y	1.122e+03
17	c	100.0	361.20	ATTS5525	A. thaliana transcribe	1.122e+03
18	c	100.0	374.18	H17884	ym33f11.61 Homo sapien	1.122e+03
19	c	100.0	374.9	AA572204	w151d01.61 Stratagene	1.122e+03
20	c	100.0	382.19	N32290	yy29f09.61 Homo sapien	1.122e+03
21	c	100.0	399.11	AA477409	zu24b08.61 Soares ovar	1.122e+03
22	c	100.0	401.19	N33865	yx74d07.61 Homo sapien	1.122e+03
23	c	100.0	411.8	AA484944	ng14g08.61 NCI CGAP L4	1.122e+03
24	c	100.0	413.10	AA455174	zw44f02.61 Soares tota	1.122e+03
25	c	100.0	417.9	AA534656	nft4e04.61 NCI CGAP Co	1.122e+03
26	c	100.0	427.11	AA632905	mp88f02.61 NCI CGAP Th	1.122e+03
27	c	100.0	427.7	AA144740	vc59g12.61 Knowles Sol	1.122e+03
28	c	100.0	430.8	AA569382	vt86b01.61 Knowles Sol	1.122e+03
29	c	100.0	442.15	AA831263	gc73f12.61 NCI CGAP GC	1.122e+03
30	c	100.0	447.10	AA425169	zw46e09.61 Soares tota	1.122e+03
31	c	100.0	448.18	H11897	ym10b10.61 Homo sapien	1.122e+03
32	c	100.0	449.19	N32414	ym83c05.61 Homo sapien	1.122e+03
33	c	100.0	456.12	M43845	232328 CD4-16 Aribidops	1.122e+03
34	c	100.0	459.19	H87695	CE151g03.61 Homo sapien	1.122e+03
35	c	100.0	468.3	M88901	CE107056 Caenorhabditis	1.122e+03
36	c	100.0	469.9	AA583428	nm38a02.61 NCI CGAP GC	1.122e+03
37	c	100.0	470.7	AA335770	vd44d08.61 Knowles Sol	1.122e+03
38	c	100.0	499.5	AA434555	ye8c07.61 Soares mouse	1.122e+03
39	c	100.0	511.19	N35184	yx83g09.61 Homo sapien	1.122e+03
40	c	100.0	519.3	T65527	cy73h06.61 Homo sapien	1.122e+03
41	c	100.0	562.12	M43855	232428 CD4-16 Aribidops	1.122e+03
42	c	100.0	562.9	AA572966	nm33b09.61 NCI CGAP L4	1.122e+03
43	c	100.0	595.3	T62521	nm504g04.61 Homo sapien	1.122e+03
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45	c	100.0	634.11	AA697513	HL02685_Sprine HL Dros	1.122e+03

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	NID	KEYWORDS	SOURCE
1	R00511	139 bp mRNA	EST			
	ye74d06.s1	Homo sapiens cDNA clone	123467 3'			
	R00511.1					
	g750247					
	EST.					
	human c106123467	library=Soares fetal liver spleen INFLS				

human clone 123647. Library= Soares fetal liver spleen INF-5 vector= pT7733 (Pharmacia) with a modified polylinker hoxB-DH108 (ampicillin resistant) primer= 21m3 RstIstet= Pac I Rstet2= Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer 15' AACGACGATCTAATATACGACATCTTTTTTTTTT 3', double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library constructed by Bento Soares and Matias Bonaldo.

Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.

REFERENCE 1 (bases 1 to 139)
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucada, T., Le, M., Lennon, G., Marra, M., Paterson, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 High quality sequence stope: 131
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (Info@Image.Lnl.gov) for further information.
 Location/Qualifiers
 FEATURES
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 /organism="Homo sapiens"
 /clone="123467"
 BASE COUNT 47 a 35 c 26 g 31 t
 ORIGIN
 Query Match 100.0%; Score 9; DB 3; Length 139;
 Best Local Similarity 100.0%; Pred. No. 1.22e+03;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 TTCTGAGAA 35
 |||||||||
 Cp 9 ttctcgaa 1

RESULT 2
 LOCUS AA368477 224 bp mRNA EST 21-APR-1997
 DEFINITION EST79880 Placenta I Homo sapiens cDNA similar to NADH-ubiquinone oxidoreductase, B22 subunit, mRNA sequence.
 ACCESSION AA368477
 NID g2020921
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 224)
 Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fulcher, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weissman, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-ai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Georghiou, N.S., Glodok, A., Guehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Li, Y., Bedarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dime, D., Feng, D.-F., Ferris, A., Fischer, G., Hastings, G.A., He, M.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wang, J., Xu, C., Yu, G.L., Ruben, S.M.,

Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
 Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
 Nature 377 (6547 suppl), 3-174 (1995)
 JOURNAL 96026280
 MEDLINE
 COMMENT Other ESTs: THC128658
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tcdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.
 Location/Qualifiers
 FEATURES
 source 1.224
 /organism="Homo sapiens"
 /note="Organ: placenta; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: EcoRI"
 /db_xref="ATCC (inhost):173295"
 /db_xref="taxon:9606"
 /clone_lib="Placenta 1"
 /tissue_type="Placenta"
 /dev stage="fetus"
 <1..>224
 BASE COUNT 64 a 53 c 58 g 48 t 1 others
 ORIGIN
 Query Match 100.0%; Score 9; DB 5; Length 224;
 Best Local Similarity 100.0%; Pred. No. 1.22e+03;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 168 TTCTGAGAA 176
 |||||||||
 Cy 1 ttctcgaa 9

RESULT 3
 LOCUS HUM506E05B 241 bp mRNA EST 12-DEC-1995
 DEFINITION Human placenta cDNA 5'-end GEN-506E05, mRNA sequence.
 ACCESSION D78718
 NID g1180591
 KEYWORDS EST; EST (expressed sequence tag); Human placenta.
 SOURCE Homo sapiens placenta cDNA to mRNA, clone_lib=human placenta polyA+.
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 241)
 Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shinada, Y., Shinomiya, H., Takachi, A., Takeda, S., Matanabe, T., Takahashi, E., Hirai, Y., Maekawa, H., Shin, S. and Nakamura, Y.
 Large-scale sequencing project at Osaka Gen Research Institute
 Unpublished (1995)
 JOURNAL 2 (bases 1 to 241)
 REFERENCE
 AUTHORS Fujiwara, T.
 TITLE Direct Submission
 JOURNAL Submitted (07-NOV-1995) to the DDBJ/EMBL/GenBank databases. Teutonu

Jul 10 12:36

/home/fuller/jul1898/US08963288.SFQ.txt

5

Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co., Ltd, 463-10 Kagasuno Kawanchi-cho, Tokushima, Tokushima 771-01, Japan
Submitted (7-Nov-1995) to DDBJ by:

Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical CO., Ltd
463-10 Kagasuno Kawanchi-cho
Tokushima, Tokushima
771-01

Japan
Phone: 0886-65-2888
Fax: 0886-37-1035.

FEATURES
source

1. .241
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="human placenta polyA+"
/tissue_type="Placenta"
BASE COUNT 66 a 54 c 45 g 71 t 5 others
ORIGIN

Query Match 100.0%; Score 9; DB 6; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.22e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 202 TTCTCAGAA 210

|||||
Cc 9 ttctcagaa 1

RESULT 4
LOCUS AA831260 250 bp mRNA EST 20-FEB-1998
DEFINITION oc3f407.e1 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:1355365
similar to SW:5111_HUMAN P31949 CALGIZARIN; , mRNA sequence.
ACCESSION AA831260
NID 92904359
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 250)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonald, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium, lml.ac:1101.gov/btrp/image/image.html

FEATURES
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 247.
Location/Qualifiers

Jul 10 12:36

/home/fuller/jul1898/US08963288.SFQ.txt

6

source

1. .250
/organism="Homo sapiens"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-GTTCACATCTGAACTGCGAGCGCCCTCATTTTCTTTTCTTTT-
3']. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT733 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonald."

/db_xref="taxon:9606"
/clone_lib="NCI CGAP GCBI"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
BASE COUNT 60 a 54 c 60 g 76 t
ORIGIN

Query Match 100.0%; Score 9; DB 15; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.22e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 14 TTCTCAGAA 22

|||||
Qy 1 ttctcagaa 9

RESULT 5
LOCUS C03864 273 bp mRNA EST 24-JUL-1996
DEFINITION Human Heart cDNA, clone 3NH2C307, mRNA sequence.
ACCESSION C03864
NID 91467115
KEYWORDS EST; EST(expressed sequence tag).
SOURCE Homo sapiens Adult Heart cDNA to mRNA.
ORGANISM Homo sapiens

Eukaryota; Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae;
Homo.

REFERENCE 1 (bases 1 to 273)
AUTHORS Tanaka, T., Ogiwara, A., Uchiyama, I., Takagi, T., Yazaki, Y. and
Nakamura, Y.

TITLE Construction of a normalized directionally cloned cDNA library from
adult heart and analysis of 3040 clones by partial sequencing
JOURNAL Genomics 35 (1), 231-235 (1996)

MEDLINE 96299762
REFERENCE 2 (bases 1 to 273)
AUTHORS Nakamura, Y.
JOURNAL Direct Submission
Submitted (22-FEB-1996) to the DDBJ/EMBL/GenBank databases. Yusuke
Nakamura, Institute of Medical Science, the University of Tokyo,
Laboratory of Molecular Medicine; 4-6-1, Shirokanedai, Minato-ku,
Tokyo 108, Japan (E-mail: yusuke@elms.u-tokyo.ac.jp,
Tel: 81-3-5449-5372, Fax: 81-3-5449-5433)

FEATURES
source
1. .273
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/dev_stage="Adult"
/tissue_type="Heart"

BASE COUNT 70 a 60 c 52 g 81 t 10 others
ORIGIN

Query Match 100.0%; Score 9; DB 6; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.22e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 149 TTCTCGAA 157
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Cp 9 ttctcgaa 1

RESULT 6
LOCUS ATTS5974 279 bp RNA EST 05-MAR-1996
DEFINITION A. thaliana transcribed sequence; clone TAP0378, 5' end, mRNA sequence.
ACCESSION F19935
NID q1215897
KEYWORDS EST; expressed sequence tag; partial cDNA sequence.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryotes; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Caprales; Brassicaceae; Arabidopsis.
1 (bases 1 to 279)
Cooke, R., Lande, M., Raynal, M. and Delseny, M.
Direct Submision
Submitted (04-MAR-1996) CNRS, GDR-1003 ACS, INRA, Laboratoire de
Biologie Moléculaire, BP 27, 31326 Castanet-Tolosan cedex, France.
E-mail: gdr-sygetoulouse.inra.fr. On behalf of: Université,
Perpignan Physiologie et Biologie des plantes, Avenue de Villeneuve
66 025 Perpignan, France. E-mail: cooke@univ-perp.fr
2 (bases 1 to 279)
CNRS.

REFERENCE
AUTHORS The Arabidopsis thaliana transcribed genome: the GDR cDNA program
JOURNAL Unpublished.
COMMENT Cloning vector: Lambda ZAP11;
Physiological conditions: cycling cells.
full automatic.
FEATURES
source
1. 279
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="TAP0378"
/issue_type="cell suspension culture of ecotype columbia"
/clone_id="Ac16H"
BASE COUNT 109 a 46 c 51 g 73 t
ORIGIN

Query Match 100.0%; Score 9; DB 20; Length 279;
Best Local Similarity 100.0%; Pred. No. 1.22e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 67 TTCTCGAA 75
|||||
Cp 1 ttctcgaa 9

RESULT 7
LOCUS T06862 289 bp mRNA EST 30-JUN-1993
DEFINITION EST04751 Homo sapiens cDNA clone HBEA09.
ACCESSION T06862
NID g318011
KEYWORDS EST.

SOURCE Human clone=HBEA09 Library=Fetal brain, Stratagene (cat#936206)
Vector=LambdaZAP-II primer=M13-21 17-18 wk gestation, female;
oligo-dT + random primed cDNA synthesis; lambdaZAP-II vector, 1.0kb
average, insert size.
ORGANISM Homo sapiens
Eukaryotes; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Primates; Haplorhina; Catarrhini; Homidae.
1 (bases 1 to 289)
Adams, M.D., Kerlavage, A.R., Fields, C. and Venter, J.C.
3400 Expressed Sequence Tags Identify Diversity of Transcripts from
Human Brain
Nature Genet. 4, 256-267 (1993)

JOURNAL
COMMENT
Contact: Adams, MD
The Institute for Genomic Research
932 Clopper Road, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: mdadams@igf.org
Location/Qualifiers
1. 289
/organism="Homo sapiens"
/clone="HBEA09"

BASE COUNT 94 a 44 c 65 g 81 t 5 others
ORIGIN

Query Match 100.0%; Score 9; DB 3; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.22e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 88 TTCTCGAA 96
|||||
Cp 9 ttctcgaa 1

RESULT 8
LOCUS R01843 300 bp mRNA EST 31-MAR-1995
DEFINITION yeb4a10.al Homo sapiens cDNA clone 124410 3' similar to gb:A06977
SERUM ALBUMIN PRECURSOR (HUMAN).
ACCESSION R01843
NID g751579
KEYWORDS EST.
SOURCE human clone=124410 library=Soares fetal liver spleen INELS
vector=PT73D (Pharmacia) with a modified polylinker host=DH10B
(ampicillin resistant) primer=-21m13 Ratel=2Pac I Ratel2=Eco RI
liver and spleen from a 20 week-post conception male fetus. 1st
strand cDNA was primed with a Pac I - oligo(dT) primer 15'
AATCGACATTTATTAAGATCTTTTTTTTTTTTTTTT 3'), double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
I and cloned into the Pac I and Eco RI sites of the modified pT73
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fátima Bonaldo.
ORGANISM Homo sapiens
Eucaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 300)
Hillier, L., Clark, N., Dubuque, T., Ellington, K., Hawking, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaekis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)

TITLE
JOURNAL
COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
High quality sequence strops: 217
Source: IMAGE Consortium, LIND
This clone is available royalty-free through LIND; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
source
1. .300
/organism="Homo sapiens"
/clone="124410"

BASE COUNT 65 a 70 c 67 g 96 t 2 others

ORIGIN
Query Match 100.0%; Score 9; DB 3; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.22e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 171 TTCTCAGAA 179
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Cp 9 ttctcagaa 1

RESULT 9
LOCUS AA35753 311 bp mRNA EST 21-APR-1997
DEFINITION EST176867 Pineal gland II Homo sapiens cDNA 5' end, mRNA sequence.
ACCESSION AA35753
NID g2018301
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
Homo.
1 (bases 1 to 311)
REFERENCE
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulcher,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Val,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,M.M., Fritcham,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaro,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y.,
Bedarick,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dinke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meisner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence

TITLE
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT Other_ESTs: THC161028
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES
source
1. .311
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/note="Organ: pineal body; Vector: pBluescript SK-
Site 1: BcoRI; Site 2: XhoI"
/db_xref="ATCC (inhost):170642"
/db_xref="taxon:9606"
/clone_lib="Pineal gland II"
/dev_stage="adult"

BASE COUNT 82 a 51 c 55 g 122 t 1 others

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.22e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 116 TTCTCAGAA 124
|||||||

Cp 9 ttctcagaa 1

RESULT 10
LOCUS AA345236 314 bp mRNA EST 21-APR-1997
DEFINITION EST151263 Gall bladder II Homo sapiens cDNA 5' end, mRNA sequence.
ACCESSION AA345236
NID g1997502
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
Homo.
1 (bases 1 to 314)
REFERENCE
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulcher,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Val,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitchhugh,M.M., Fritcham,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaro,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y.,
Bedarick,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dinke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meisner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence

TITLE
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT Other_ESTs: THC178905


```

RESULT 15
LOCUS CELK074C5F 360 bp mRNA EST 06-JAN-1997
DEFINITION C.elegans cDNA clone yk74c5 : 5' end, single read, mRNA sequence.
ACCESSION D74048
NID 91119832
KEYWORDS EST; EST(expressed sequence tag);
SOURCE Caenorhabditis elegans (strain:N2) embryo Hermaphrodite embryo cDNA
to mRNA, clone lib::Yuji kohara unpublished cDNA.
ORGANISM Caenorhabditis elegans
Eukaryoteae; mitochondria eukaryotes; Metazoa; Nematoda;
Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 360)
AUTHORS Kohara,Y., Motohashi,T., Tabara,H., Sugimoto,A., Watanabe,H. and
Nishigaki,A.
TITLE Toward an expression map of the C.elegans genome
JOURNAL Unpublished (1995)
REFERENCE 2 (bases 1 to 360)
AUTHORS Kohara,Y.
JOURNAL Direct Submission
Submitted (23-AUG-1995) to the DDBJ/EMBL/GenBank databases. Yuji
Kohara, National Institute of Genetics, Gene Library Lab; Yata
1111, Mishima, Shizuoka 411, Japan (E-mail:ykohara@lab.nig.ac.jp,
Tel:0559-81-6854, Fax:0559-81-6855)
FEATURES
    source
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            /strain="N2"
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            /clone_lib="Yuji kohara unpublished cDNA"
            /dev_stage="embryo"
            /sex="Hermaphrodite"
            /tissue_type="embryo"
BASE COUNT 104 a 76 c 68 g 107 t 5 others
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.22e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 80 TTCTCAGAA 88
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Cp 9 ttctcagaa 1

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 Job time : 83 secs.

Jul 10 12:36

/home/fuller/fu1898/US08963288 SEQ.rst

13

FEATURES

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality.

FEATURES

Location/Qualifiers
1. 324
/organism="Homo sapiens"
/clone="158942"

BASE COUNT 82 a 82 c 83 g 76 t 1 others
ORIGIN

Query Match 100.0%; Score 9; DB 14; Length 324;
Best Local Similarity 100.0%; Pred. No. 1.22e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 TTCTCAGAA 111
|||||

Cp 9 ttctcagaa 1

RESULT 13
LOCUS H88997 325 bp mRNA EST 22-NOV-1995
DEFINITION yw26503.t1 Homo sapiens cDNA clone 253325 5'.
ACCESSION H88997
NID g1071257
KEYWORDS
SOURCE human clone=253325 primer=M13RP1 library=Morton Fetal Cochlea
vector=pBluescript SK- host=SO4R cells (kanamycin resistant)
Reitell-Ecorti Reitell2-XhoI The cDNA was oligo (dT) primed with an
XhoI restriction enzyme recognition site and an 18 base poly dT
sequence. For the 5' end, the synthesized cDNA termini were
treated with T4 DNA polymerase and EcoRI adaptors were ligated to
the blunt ends. adaptor linker: GAATTCGCCACGAG.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 325)

REFERENCE

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevasaki, E.,
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
Washington University School of Medicine
Unpublished (1995)

TITLE

JOURNAL

COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 278
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the

Jul 10 12:36

/home/fuller/fu1898/US08963288 SEQ.rst

14

FEATURES

IMAGE Consortium (info@image.llnl.gov) for further information.

Location/Qualifiers
1. 325
/organism="Homo sapiens"
/clone="253325"

BASE COUNT 95 a 53 c 64 g 111 t 2 others
ORIGIN

Query Match 100.0%; Score 9; DB 19; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.22e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 89 TTCTCAGAA 97
|||||

Cy 1 ttctcagaa 9

RESULT 14
LOCUS C60411 360 bp mRNA EST 29-AUG-1997
DEFINITION C.elegans cDNA clone yk200a8 : 5' end, single read, mRNA sequence.
ACCESSION C60411
NID g2419116
KEYWORDS EST; EST (expressed sequence tag).
SOURCE Caenorhabditis elegans (strain: C61489 him-8(e1489)) varied
hermaphrodite, male whole animal cDNA to mRNA, clone_lib:Yoji
Kohara unpublished cDNA library clone:yk200a8.
Caenorhabditis elegans

ORGANISM
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Pelodierinae; Caenorhabditis.
1 (sites)

REFERENCE
Kohara, Y., Motohashi, T., Tabara, H., Shin-i, T., Watanabe, H.,
Sano, M., Miyata, A., Ohba, T., Mitani, Y., Uesugi, H., Sugitani, I.,
Obara, M., Sugimoto, A., Iida, K. and Nishigaki, A.
Expression map of the C.elegans genome
Unpublished (1997)
2 (bases 1 to 360)

TITLE
JOURNAL
AUTHORS
TITLE Direct Submission
Submitted (23-JUL-1997) to the DDBJ/EMBL/GenBank databases. Yuji
Kohara, National Institute of Genetics, Gene Network Lab; Yata
1111, Mishima, Shizuoka 411, Japan (E-mail: yk@kohara.nig.ac.jp,
Tel: +81-559-81-6854, Fax: +81-559-81-6855)

FEATURES

SOURCE

Location/Qualifiers
1. 360
/organism="Caenorhabditis elegans"
/strain="C61489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="yk200a8"
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/dev_stage="varied"
/sex="hermaphrodite, male"
/tissue type="whole animal"

BASE COUNT 103 a 97 c 72 g 86 t 2 others
ORIGIN

Query Match 100.0%; Score 9; DB 10; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.22e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 289 TTCTCAGAA 297
|||||

Cy 1 ttctcagaa 9